GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: October 2, 2003, 15:45:58 ; Search time 3 Seconds
(without alignments)
1.084 Million cell updates/sec

Title: us-09-676-436-3
Perfect score: 20
Sequence: 1 agggattcaggggttccagc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 7024 seqs, 81329 residues

Total number of hits satisfying chosen parameters: 14040

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 32 summaries

Database : rnpb.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	20	100.0	20	1	US-10-371-474-12	Sequence 12, Appl
c	2	13	65.0	20	1	US-10-371-474-64	Sequence 64, Appl
c	3	12.8	64.0	19	1	US-09-953-562-3	Sequence 3, Appli
c	4	12.8	64.0	24	1	US-09-953-562-25	Sequence 25, Appl
	5	12.4	62.0	14	1	US-08-591-486B-72	Sequence 72, Appl
c	6	11.2	56.0	24	1	US-09-953-562-24	Sequence 24, Appl
c	7	10	50.0	20	1	US-10-371-474-61	Sequence 61, Appl
	8	9	45.0	29	1	US-09-953-562-1	Sequence 1, Appli
	9	8.8	44.0	14	1	US-08-591-486B-68	Sequence 68, Appl
	10	8.8	44.0	18	1	US-08-591-486B-67	Sequence 67, Appl
c	11	8.6	43.0	37	1	US-09-955-518-11	Sequence 11, Appl
c	12	8.4	42.0	10	1	US-09-953-562-26	Sequence 26, Appl
	13	8.4	42.0	10	1	US-09-989-994-1270	Sequence 1270, Ap
	14	8.4	42.0	10	1	US-09-989-994-1275	Sequence 1275, Ap
	15	8.4	42.0	10	1	US-09-989-994-1337	Sequence 1337, Ap
	16	8.4	42.0	10	1	US-09-990-186-1270	Sequence 1270, Ap
	17	8.4	42.0	10	1	US-09-990-186-1275	Sequence 1275, Ap
	18	8.4	42.0	10	1	US-09-990-186-1337	Sequence 1337, Ap
	19	8.4	42.0	10	1	US-10-330-627-435	Sequence 435, App
	20	8.4	42.0	10	1	US-10-330-627-1496	Sequence 1496, Ap
	21	8.4	42.0	10	1	US-10-330-627-1546	Sequence 1546, Ap
	22	8.4	42.0	10	1	US-09-989-789-1270	Sequence 1270, Ap
	23	8.4	42.0	10	1	US-09-989-789-1275	Sequence 1275, Ap
	24	8.4	42.0	10	1	US-09-989-789-1337	Sequence 1337, Ap
	25	8.2	41.0	30	1	US-08-591-486B-43	Sequence 43, Appl
	26	8	40.0	10	1	US-10-330-627-588	Sequence 588, App
c	27	8	40.0	10	1	US-10-033-145-524	Sequence 524, App
	28	8	40.0	10	1	US-10-033-145-765	Sequence 765, App
	29	8	40.0	10	1	US-10-033-145-1337	Sequence 1337, Ap
	30	8	40.0	20	1	US-10-371-474-17	Sequence 17, Appl
	31	7.8	39.0	16	1	US-08-591-486B-163	Sequence 163, App
c	32	7.4	37.0	9	1	US-09-955-518-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-10-371-474-12/c
; Sequence 12, Application US/10371474
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; APPLICANT: William Gaarde
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF MEKK4 EXPRESSION
; FILE REFERENCE: RTS-0169
; CURRENT APPLICATION NUMBER: US/10/371,474
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US/09/676,436
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-371-474-12

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       3314 AGGGATTCAGGGGTTCCAGC 3333
              ||||||||||||||||||||
Db         20 AGGGATTCAGGGGTTCCAGC 1
```

RESULT 2
US-10-371-474-64/c
; Sequence 64, Application US/10371474
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; APPLICANT: William Gaarde
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF MEKK4 EXPRESSION
; FILE REFERENCE: RTS-0169
; CURRENT APPLICATION NUMBER: US/10/371,474
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US/09/676,436
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 64
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-371-474-64

Query Match 65.0%; Score 13; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.092;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       3321 CAGGGGTTCCAGC 3333
              |||||||||||||
Db         13 CAGGGGTTCCAGC 1
```

RESULT 3
US-09-953-562-3/c
; Sequence 3, Application US/09953562
; GENERAL INFORMATION:
; APPLICANT: ZERIA PHARMACEUTICALS CO., LTD.

```
;  TITLE OF INVENTION: METHOD OF SCREENING A DRUG FOR TREATMENT OF SQUAMOUS
;  TITLE OF INVENTION:  CELL CARCINOMA
;  FILE REFERENCE: E6114-01
;  CURRENT APPLICATION NUMBER: US/09/953,562
;  CURRENT FILING DATE:  2003-02-24
;  PRIOR APPLICATION NUMBER: JP 2001-083352
;  PRIOR FILING DATE: 2001-03-22
;  NUMBER OF SEQ ID NOS: 27
; SEQ ID NO 3
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: FGFR3 mutagenic oligonucleotide
US-09-953-562-3

  Query Match             64.0%;  Score 12.8;  DB 1;  Length 19;
  Best Local Similarity   87.5%;  Pred. No. 0.11;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3314 AGGGATTCAGGGGTTC 3329
              |||||| ||||||| |
Db         18 AGGGATGCAGGGGTAC 3


RESULT 4
US-09-953-562-25/c
; Sequence 25, Application US/09953562
; GENERAL INFORMATION:
;  APPLICANT: ZERIA PHARMACEUTICALS CO., LTD.
;  TITLE OF INVENTION: METHOD OF SCREENING A DRUG FOR TREATMENT OF SQUAMOUS
;  TITLE OF INVENTION:  CELL CARCINOMA
;  FILE REFERENCE: E6114-01
;  CURRENT APPLICATION NUMBER: US/09/953,562
;  CURRENT FILING DATE:  2003-02-24
;  PRIOR APPLICATION NUMBER: JP 2001-083352
;  PRIOR FILING DATE: 2001-03-22
;  NUMBER OF SEQ ID NOS: 27
; SEQ ID NO 25
;   LENGTH: 24
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-953-562-25

  Query Match             64.0%;  Score 12.8;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 0.13;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3314 AGGGATTCAGGGGTTC 3329
              |||||| ||||||| |
Db         21 AGGGATGCAGGGGTAC 6


RESULT 5
US-08-591-486B-72
; Sequence 72, Application US/08591486B
;  GENERAL INFORMATION:
;    APPLICANT:  Schlingensiepen, Georg F
;    APPLICANT:  Schlingensiepen, Reimar
;    APPLICANT:  Schlingensiepen, Karl-Hermann
;    APPLICANT:  Gotingen, Wolfgang Brysch
;    TITLE OF INVENTION:  A Pharmaceutical Composition
;    TITLE OF INVENTION:  Comprising Antisense-Nucleic Acid for Prevention and/or Treatm
;    TITLE OF INVENTION:  of Neuronal Injury, Degeneration and Cell Death and for the
;    TITLE OF INVENTION:  Treatment of Neoplasms
;    NUMBER OF SEQUENCES:  185
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jacobson, Price, Holman & Stern
;      STREET:  400 Seventh Street, N.W.
;      CITY:  Washington, D.C
;      COUNTRY:  U.S.A.
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/591,486B
;      FILING DATE:  11-JAN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 93111059.7
;      FILING DATE:  10-JUL-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP94/02218
;      FILING DATE:  6-JUL-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Player, William E.
;      REGISTRATION NUMBER:  31,409
;      REFERENCE/DOCKET NUMBER:  10496/P60122
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 638-6666
;      TELEFAX:  (202) 393-9350
;      TELEX:  RCA 248593 IDEA UR
;  INFORMATION FOR SEQ ID NO:  72:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  14 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
;    ANTI-SENSE:  YES
US-08-591-486B-72

  Query Match             62.0%;  Score 12.4;  DB 1;  Length 14;
  Best Local Similarity   92.9%;  Pred. No. 0.16;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3318 ATTCAGGGGTTCCA 3331
              ||||||| ||||||
Db          1 ATTCAGGCGTTCCA 14


RESULT 6
US-09-953-562-24/c
; Sequence 24, Application US/09953562
; GENERAL INFORMATION:
;  APPLICANT: ZERIA PHARMACEUTICALS CO., LTD.
;  TITLE OF INVENTION: METHOD OF SCREENING A DRUG FOR TREATMENT OF SQUAMOUS
;  TITLE OF INVENTION:  CELL CARCINOMA
;  FILE REFERENCE: E6114-01
;  CURRENT APPLICATION NUMBER: US/09/953,562
;  CURRENT FILING DATE:  2003-02-24
;  PRIOR APPLICATION NUMBER: JP 2001-083352
;  PRIOR FILING DATE: 2001-03-22
;  NUMBER OF SEQ ID NOS: 27
; SEQ ID NO 24
;   LENGTH: 24
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-953-562-24

  Query Match             56.0%;  Score 11.2;  DB 1;  Length 24;
  Best Local Similarity   81.2%;  Pred. No. 0.94;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3314 AGGGATTCAGGGGTTC 3329
              |||||| | ||||| |
Db         21 AGGGATGCCGGGGTAC 6


RESULT 7
US-10-371-474-61/c
; Sequence 61, Application US/10371474
; GENERAL INFORMATION:
```

```
;  APPLICANT: Donna T. Ward
;  APPLICANT:  William Gaarde
;  APPLICANT:  Brett P. Monia
;  APPLICANT:  Jacqueline Wyatt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF MEKK4 EXPRESSION
;  FILE REFERENCE: RTS-0169
;  CURRENT APPLICATION NUMBER: US/10/371,474
;  CURRENT FILING DATE:  2003-02-21
;  PRIOR APPLICATION NUMBER: US/09/676,436
;  PRIOR FILING DATE: 2000-09-29
;  NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 61
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-371-474-61

  Query Match             50.0%;  Score 10;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.7;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3314 AGGGATTCAG 3323
              ||||||||||
Db         13 AGGGATTCAG 4


RESULT 8
US-09-953-562-1
; Sequence 1, Application US/09953562
; GENERAL INFORMATION:
;  APPLICANT: ZERIA PHARMACEUTICALS CO., LTD.
;  TITLE OF INVENTION: METHOD OF SCREENING A DRUG FOR TREATMENT OF SQUAMOUS
;  TITLE OF INVENTION:  CELL CARCINOMA
;  FILE REFERENCE: E6114-01
;  CURRENT APPLICATION NUMBER: US/09/953,562
;  CURRENT FILING DATE:  2003-02-24
;  PRIOR APPLICATION NUMBER: JP 2001-083352
;  PRIOR FILING DATE: 2001-03-22
;  NUMBER OF SEQ ID NOS: 27
; SEQ ID NO 1
;   LENGTH: 29
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Upstream primer
US-09-953-562-1

  Query Match             45.0%;  Score 9;  DB 1;  Length 29;
  Best Local Similarity   70.6%;  Pred. No. 16;
  Matches   12;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       3315 GGGATTCAGGGGTTCCA 3331
              || |||||  |  ||||
Db          2 GGAATTCAACGCGTCCA 18


RESULT 9
US-08-591-486B-68
; Sequence 68, Application US/08591486B
;  GENERAL INFORMATION:
;    APPLICANT:  Schlingensiepen, Georg F
;    APPLICANT:  Schlingensiepen, Reimar
;    APPLICANT:  Schlingensiepen, Karl-Hermann
;    APPLICANT:  Gotingen, Wolfgang Brysch
;    TITLE OF INVENTION:  A Pharmaceutical Composition
;    TITLE OF INVENTION:  Comprising Antisense-Nucleic Acid for Prevention and/or Treatm
;    TITLE OF INVENTION:  of Neuronal Injury, Degeneration and Cell Death and for the
;    TITLE OF INVENTION:  Treatment of Neoplasms
;    NUMBER OF SEQUENCES:  185
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jacobson, Price, Holman & Stern
;      STREET:  400 Seventh Street, N.W.
;      CITY:  Washington, D.C
;      COUNTRY:  U.S.A.
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/591,486B
;      FILING DATE:  11-JAN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 93111059.7
;      FILING DATE:  10-JUL-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP94/02218
;      FILING DATE:  6-JUL-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Player, William E.
;      REGISTRATION NUMBER:  31,409
;      REFERENCE/DOCKET NUMBER:  10496/P60122
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 638-6666
;      TELEFAX:  (202) 393-9350
;      TELEX:  RCA 248593 IDEA UR
;  INFORMATION FOR SEQ ID NO:  68:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  14 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
;    ANTI-SENSE:  YES
US-08-591-486B-68

  Query Match             44.0%;  Score 8.8;  DB 1;  Length 14;
  Best Local Similarity   83.3%;  Pred. No. 13;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3316 GGATTCAGGGGT 3327
              || |||||| ||
Db          3 GGTTTCAGGAGT 14


RESULT 10
US-08-591-486B-67
; Sequence 67, Application US/08591486B
;  GENERAL INFORMATION:
;    APPLICANT:  Schlingensiepen, Georg F
;    APPLICANT:  Schlingensiepen, Reimar
;    APPLICANT:  Schlingensiepen, Karl-Hermann
;    APPLICANT:  Gotingen, Wolfgang Brysch
;    TITLE OF INVENTION:  A Pharmaceutical Composition
;    TITLE OF INVENTION:  Comprising Antisense-Nucleic Acid for Prevention and/or Tr
;    TITLE OF INVENTION:  of Neuronal Injury, Degeneration and Cell Death and for th
;    TITLE OF INVENTION:  Treatment of Neoplasms
;    NUMBER OF SEQUENCES:  185
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jacobson, Price, Holman & Stern
;      STREET:  400 Seventh Street, N.W.
;      CITY:  Washington, D.C
;      COUNTRY:  U.S.A.
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/591,486B
;      FILING DATE:  11-JAN-1995
```

```
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 93111059.7
;      FILING DATE:  10-JUL-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP94/02218
;      FILING DATE:  6-JUL-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Player, William E.
;      REGISTRATION NUMBER:  31,409
;      REFERENCE/DOCKET NUMBER:  10496/P60122
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 638-6666
;      TELEFAX:  (202) 393-9350
;      TELEX:  RCA 248593 IDEA UR
;  INFORMATION FOR SEQ ID NO:  67:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
;    ANTI-SENSE:  YES
US-08-591-486B-67

  Query Match             44.0%;  Score 8.8;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 15;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3317 GATTCAGGGGTT 3328
              | |||||| |||
Db          1 GTTTCAGGAGTT 12


RESULT 11
US-09-955-518-11/c
; Sequence 11, Application US/09955518
; Patent No. US20020042138A1
; GENERAL INFORMATION:
;  APPLICANT: Townes, Tim M.
;  APPLICANT:  Donze, David
;  TITLE OF INVENTION: DELTA-ERYTHROID KRUPPEL-LIKE FACTORS AND
;  TITLE OF INVENTION:  METHODS OF USE
;  FILE REFERENCE: 05118.000802
;  CURRENT APPLICATION NUMBER: US/09/955,518
;  CURRENT FILING DATE:  2001-09-18
;  PRIOR APPLICATION NUMBER: 60/019,769
;  PRIOR FILING DATE: 1996-06-14
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 37
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:\ No. US20020042138A1e =
;   OTHER INFORMATION: synthetic construct
US-09-955-518-11

  Query Match             43.0%;  Score 8.6;  DB 1;  Length 37;
  Best Local Similarity   73.3%;  Pred. No. 30;
  Matches   11;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3314 AGGGATTCAGGGGTT 3328
              |||| |||| |||
Db         20 AGGGTTTCATTAGTT 6


RESULT 12
US-09-953-562-26/c
; Sequence 26, Application US/09953562
; GENERAL INFORMATION:
;  APPLICANT: ZERIA PHARMACEUTICALS CO., LTD.
;  TITLE OF INVENTION: METHOD OF SCREENING A DRUG FOR TREATMENT OF SQUAMOUS
;  TITLE OF INVENTION:  CELL CARCINOMA
;  FILE REFERENCE: E6114-01
;  CURRENT APPLICATION NUMBER: US/09/953,562
;  CURRENT FILING DATE:  2003-02-24
;  PRIOR APPLICATION NUMBER: JP 2001-083352
;  PRIOR FILING DATE: 2001-03-22
;  NUMBER OF SEQ ID NOS: 27
; SEQ ID NO 26
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-953-562-26

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 18;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3316 GGATTCAGGG 3325
              |||| |||||
Db         10 GGATGCAGGG 1


RESULT 13
US-09-989-994-1270
; Sequence 1270, Application US/09989994
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,994
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1270
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-994-1270

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 18;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3314 AGGGATTCAG 3323
              | ||||||||
Db          1 ATGGATTCAG 10


RESULT 14
US-09-989-994-1275
; Sequence 1275, Application US/09989994
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,994
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1275
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-994-1275
```

```
  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 18;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3314 AGGGATTCAG 3323
             | ||||||||
Db          1 ATGGATTCAG 10


RESULT 15
US-09-989-994-1337
; Sequence 1337, Application US/09989994
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,994
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1337
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-994-1337

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 18;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3314 AGGGATTCAG 3323
             | ||||||||
Db          1 ATGGATTCAG 10


RESULT 16
US-09-990-186-1270
; Sequence 1270, Application US/09990186
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.21 / S11-US3
;  CURRENT APPLICATION NUMBER: US/09/990,186
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1270
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-990-186-1270

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 18;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3314 AGGGATTCAG 3323
             | ||||||||
Db          1 ATGGATTCAG 10


RESULT 17
US-09-990-186-1275
; Sequence 1275, Application US/09990186
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.21 / S11-US3
;  CURRENT APPLICATION NUMBER: US/09/990,186
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1275
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-990-186-1275

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 18;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3314 AGGGATTCAG 3323
             | ||||||||
Db          1 ATGGATTCAG 10


RESULT 18
US-09-990-186-1337
; Sequence 1337, Application US/09990186
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.21 / S11-US3
;  CURRENT APPLICATION NUMBER: US/09/990,186
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1337
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-990-186-1337

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 18;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3314 AGGGATTCAG 3323
             | ||||||||
Db          1 ATGGATTCAG 10


RESULT 19
US-10-330-627-435
; Sequence 435, Application US/10330627
; GENERAL INFORMATION:
;  APPLICANT: Velculescu, Victor E.
;  APPLICANT:  Kinzler, Kenneth W
;  APPLICANT:  Vogelstein, Bert
;  TITLE OF INVENTION: Human Transcriptomes
;  FILE REFERENCE: 001107.00319
;  CURRENT APPLICATION NUMBER: US/10/330,627
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 09/448,480
;  PRIOR FILING DATE: 1999-11-24
;  NUMBER OF SEQ ID NOS: 1564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 435
```

```
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-330-627-435

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 18;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3322 AGGGGTTCCA 3331
              |||| |||||
Db          1 AGGGCTTCCA 10


RESULT 20
US-10-330-627-1496
; Sequence 1496, Application US/10330627
; GENERAL INFORMATION:
;  APPLICANT: Velculescu, Victor E.
;  APPLICANT:  Kinzler, Kenneth W
;  APPLICANT:  Vogelstein, Bert
;  TITLE OF INVENTION: Human Transcriptomes
;  FILE REFERENCE: 001107.00319
;  CURRENT APPLICATION NUMBER: US/10/330,627
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 09/448,480
;  PRIOR FILING DATE: 1999-11-24
;  NUMBER OF SEQ ID NOS: 1564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1496
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-330-627-1496

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 18;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3322 AGGGGTTCCA 3331
              |||| |||||
Db          1 AGGGCTTCCA 10


RESULT 21
US-10-330-627-1546
; Sequence 1546, Application US/10330627
; GENERAL INFORMATION:
;  APPLICANT: Velculescu, Victor E.
;  APPLICANT:  Kinzler, Kenneth W
;  APPLICANT:  Vogelstein, Bert
;  TITLE OF INVENTION: Human Transcriptomes
;  FILE REFERENCE: 001107.00319
;  CURRENT APPLICATION NUMBER: US/10/330,627
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 09/448,480
;  PRIOR FILING DATE: 1999-11-24
;  NUMBER OF SEQ ID NOS: 1564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1546
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-330-627-1546

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 18;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3322 AGGGGTTCCA 3331
              |||| |||||
Db          1 AGGGCTTCCA 10


RESULT 22
US-09-989-789-1270
; Sequence 1270, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,789
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1270
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-789-1270

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 18;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3314 AGGGATTCAG 3323
              | ||||||||
Db          1 ATGGATTCAG 10


RESULT 23
US-09-989-789-1275
; Sequence 1275, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,789
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1275
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-789-1275

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 18;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3314 AGGGATTCAG 3323
              | ||||||||
Db          1 ATGGATTCAG 10


RESULT 24
US-09-989-789-1337
; Sequence 1337, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,789
```

```
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1337
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-789-1337

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 18;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3314 AGGGATTCAG 3323
              | ||||||||
Db          1 ATGGATTCAG 10


RESULT 25
US-08-591-486B-43
; Sequence 43, Application US/08591486B
;  GENERAL INFORMATION:
;    APPLICANT:  Schlingensiepen, Georg F
;    APPLICANT:  Schlingensiepen, Reimar
;    APPLICANT:  Schlingensiepen, Karl-Hermann
;    APPLICANT:  Gotingen, Wolfgang Brysch
;    TITLE OF INVENTION:  A Pharmaceutical Composition
;    TITLE OF INVENTION:  Comprising Antisense-Nucleic Acid for Prevention and/or Treatm
;    TITLE OF INVENTION:  of Neuronal Injury, Degeneration and Cell Death and for the
;    TITLE OF INVENTION:  Treatment of Neoplasms
;    NUMBER OF SEQUENCES:  185
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jacobson, Price, Holman & Stern
;      STREET:  400 Seventh Street, N.W.
;      CITY:  Washington, D.C
;      COUNTRY:  U.S.A.
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/591,486B
;      FILING DATE:  11-JAN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 93111059.7
;      FILING DATE:  10-JUL-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP94/02218
;      FILING DATE:  6-JUL-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Player, William E.
;      REGISTRATION NUMBER:  31,409
;      REFERENCE/DOCKET NUMBER:  10496/P60122
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 638-6666
;      TELEFAX:  (202) 393-9350
;      TELEX:  RCA 248593 IDEA UR
;  INFORMATION FOR SEQ ID NO:  43:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  30 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
;    ANTI-SENSE:  YES
US-08-591-486B-43

  Query Match             41.0%;  Score 8.2;  DB 1;  Length 30;
  Best Local Similarity   76.9%;  Pred. No. 43;
  Matches   10;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3319 TTCAGGGGTTCCA 3331
              |||| || || ||
Db          8 TTCAAGGTTTTCA 20


RESULT 26
US-10-330-627-588
; Sequence 588, Application US/10330627
; GENERAL INFORMATION:
;  APPLICANT: Velculescu, Victor E.
;  APPLICANT:  Kinzler, Kenneth W
;  APPLICANT:  Vogelstein, Bert
;  TITLE OF INVENTION: Human Transcriptomes
;  FILE REFERENCE: 001107.00319
;  CURRENT APPLICATION NUMBER: US/10/330,627
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 09/448,480
;  PRIOR FILING DATE: 1999-11-24
;  NUMBER OF SEQ ID NOS: 1564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 588
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-330-627-588

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 30;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3319 TTCAGGGG 3326
              ||||||||
Db          2 TTCAGGGG 9


RESULT 27
US-10-033-145-524/c
; Sequence 524, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
;  APPLICANT: GENZYME CORPORATION
;  APPLICANT:  ROBERTS, BRUCE
;  APPLICANT:  SHANKARA, SRINIVAS
;  TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
;  FILE REFERENCE: GA0201C
;  CURRENT APPLICATION NUMBER: US/10/033,145
;  CURRENT FILING DATE:  2001-11-05
;  PRIOR APPLICATION NUMBER: PCT/US99/13800
;  PRIOR FILING DATE: 1999-06-18
;  NUMBER OF SEQ ID NOS: 2137
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 524
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-033-145-524

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 30;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3320 TCAGGGGT 3327
              ||||||||
Db          9 TCAGGGGT 2


RESULT 28
US-10-033-145-765
; Sequence 765, Application US/10033145
```

```
; Publication No. US20020151515A1
; GENERAL INFORMATION:
;  APPLICANT: GENZYME CORPORATION
;  APPLICANT:  ROBERTS, BRUCE
;  APPLICANT:  SHANKARA, SRINIVAS
;  TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
;  FILE REFERENCE: GA0201C
;  CURRENT APPLICATION NUMBER: US/10/033,145
;  CURRENT FILING DATE:  2001-11-05
;  PRIOR APPLICATION NUMBER: PCT/US99/13800
;  PRIOR FILING DATE: 1999-06-18
;  NUMBER OF SEQ ID NOS: 2137
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 765
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-033-145-765

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 30;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3324 GGGTTCCA 3331
              ||||||||
Db          3 GGGTTCCA 10


RESULT 29
US-10-033-145-1337
; Sequence 1337, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
;  APPLICANT: GENZYME CORPORATION
;  APPLICANT:  ROBERTS, BRUCE
;  APPLICANT:  SHANKARA, SRINIVAS
;  TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
;  FILE REFERENCE: GA0201C
;  CURRENT APPLICATION NUMBER: US/10/033,145
;  CURRENT FILING DATE:  2001-11-05
;  PRIOR APPLICATION NUMBER: PCT/US99/13800
;  PRIOR FILING DATE: 1999-06-18
;  NUMBER OF SEQ ID NOS: 2137
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1337
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-033-145-1337

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 30;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3319 TTCAGGGG 3326
              ||||||||
Db          2 TTCAGGGG 9


RESULT 30
US-10-371-474-17
; Sequence 17, Application US/10371474
; GENERAL INFORMATION:
;  APPLICANT: Donna T. Ward
;  APPLICANT:  William Gaarde
;  APPLICANT:  Brett P. Monia
;  APPLICANT:  Jacqueline Wyatt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF MEKK4 EXPRESSION
;  FILE REFERENCE: RTS-0169
;  CURRENT APPLICATION NUMBER: US/10/371,474
;  CURRENT FILING DATE:  2003-02-21
;  PRIOR APPLICATION NUMBER: US/09/676,436
;  PRIOR FILING DATE: 2000-09-29
;  NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 17
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-371-474-17

  Query Match             40.0%;  Score 8;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 44;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3317 GATTCAGG 3324
              ||||||||
Db          8 GATTCAGG 15


RESULT 31
US-08-591-486B-163
; Sequence 163, Application US/08591486B
;  GENERAL INFORMATION:
;    APPLICANT:  Schlingensiepen, Georg F
;    APPLICANT:  Schlingensiepen, Reimar
;    APPLICANT:  Schlingensiepen, Karl-Hermann
;    APPLICANT:  Gotingen, Wolfgang Brysch
;    TITLE OF INVENTION:  A Pharmaceutical Composition
;    TITLE OF INVENTION:  Comprising Antisense-Nucleic Acid for Prevention and/or Tr
;    TITLE OF INVENTION:  of Neuronal Injury, Degeneration and Cell Death and for th
;    TITLE OF INVENTION:  Treatment of Neoplasms
;    NUMBER OF SEQUENCES:  185
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jacobson, Price, Holman & Stern
;      STREET:  400 Seventh Street, N.W.
;      CITY:  Washington, D.C
;      COUNTRY:  U.S.A.
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/591,486B
;      FILING DATE:  11-JAN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 93111059.7
;      FILING DATE:  10-JUL-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP94/02218
;      FILING DATE:  6-JUL-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Player, William E.
;      REGISTRATION NUMBER:  31,409
;      REFERENCE/DOCKET NUMBER:  10496/P60122
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 638-6666
;      TELEFAX:  (202) 393-9350
;      TELEX:  RCA 248593 IDEA UR
;  INFORMATION FOR SEQ ID NO:  163:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  16 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
;    ANTI-SENSE:  YES
US-08-591-486B-163

  Query Match             39.0%;  Score 7.8;  DB 1;  Length 16;
  Best Local Similarity   81.8%;  Pred. No. 50;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
```

```
Qy       3314 AGGGATTCAGG 3324
             |||||| |||
Db          1 AGGGATAAAGG 11


RESULT 32
US-09-955-518-18/c
; Sequence 18, Application US/09955518
; Patent No. US20020042138A1
; GENERAL INFORMATION:
;  APPLICANT: Townes, Tim M.
;  APPLICANT:  Donze, David
;  TITLE OF INVENTION: DELTA-ERYTHROID KRUPPEL-LIKE FACTORS AND
;  TITLE OF INVENTION:  METHODS OF USE
;  FILE REFERENCE: 05118.0008U2
;  CURRENT APPLICATION NUMBER: US/09/955,518
;  CURRENT FILING DATE:  2001-09-18
;  PRIOR APPLICATION NUMBER: 60/019,769
;  PRIOR FILING DATE: 1996-06-14
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:\ No. US20020042138A1e =
;   OTHER INFORMATION: synthetic construct
US-09-955-518-18

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.3e+04;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3314 AGGGATTCA 3322
             |||| ||||
Db          9 AGGGTTTCA 1


Search completed: October  2, 2003, 15:46:01
Job time : 3 secs
```

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: October 2, 2003, 15:40:42 ; Search time 0.001 Seconds
(without alignments)
1023.400 Million cell updates/sec

Title: us-09-676-436-3
Perfect score: 20
Sequence: 1 agggattcaggggttccagc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1282 seqs, 25585 residues

Total number of hits satisfying chosen parameters: 2520

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : rni.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	10	50.0	10	1	US-07-704-288C-25	Sequence 25, Appl
c	2	10	50.0	10	1	US-08-379-259-25	Sequence 25, Appl
c	3	8.6	43.0	37	1	US-08-874-569B-11	Sequence 11, Appl
c	4	8.6	43.0	37	1	US-09-955-518-11	Sequence 11, Appl
	5	8.4	42.0	10	1	US-09-508-753B-123	Sequence 123, App
c	6	8.4	42.0	10	1	US-09-508-753B-149	Sequence 149, App
	7	8.2	41.0	30	1	US-08-899-324-21	Sequence 21, Appl
	8	8.2	41.0	30	1	US-08-329-892B-21	Sequence 21, Appl
c	9	8	40.0	8	1	US-08-859-954-239	Sequence 239, App
	10	8	40.0	10	1	US-08-590-804-20	Sequence 20, Appl
	11	8	40.0	10	1	US-09-508-753B-199	Sequence 199, App
c	12	8	40.0	10	1	US-09-508-753B-253	Sequence 253, App
c	13	7.4	37.0	9	1	US-08-899-324-6	Sequence 6, Appli
c	14	7.4	37.0	9	1	US-08-329-892B-6	Sequence 6, Appli
c	15	7.4	37.0	9	1	US-08-874-569B-18	Sequence 18, Appl
c	16	7.4	37.0	9	1	US-09-955-518-18	Sequence 18, Appl
c	17	7.4	37.0	10	1	US-07-704-288C-5	Sequence 5, Appli
c	18	7.4	37.0	10	1	US-08-379-259-5	Sequence 5, Appli
	19	7.4	37.0	10	1	US-09-508-753B-87	Sequence 87, Appl
	20	7.4	37.0	10	1	US-09-508-753B-121	Sequence 121, App
c	21	7.4	37.0	10	1	US-09-508-753B-134	Sequence 134, App
	22	7.4	37.0	10	1	US-09-508-753B-172	Sequence 172, App
c	23	7.2	36.0	37	1	US-09-508-753B-15	Sequence 15, Appl
	24	7	35.0	8	1	US-08-859-954-32	Sequence 32, Appl
c	25	7	35.0	8	1	US-08-859-954-240	Sequence 240, App
c	26	7	35.0	8	1	US-08-859-954-292	Sequence 292, App
c	27	7	35.0	8	1	US-09-063-450-8	Sequence 8, Appli
c	28	7	35.0	8	1	US-09-398-499-15	Sequence 15, Appl
	29	7	35.0	8	1	US-09-398-499-38	Sequence 38, Appl
c	30	7	35.0	10	1	US-08-590-804-25	Sequence 25, Appl
	31	7	35.0	10	1	US-09-398-499-58	Sequence 58, Appl
c	32	7	35.0	10	1	US-09-508-753B-22	Sequence 22, Appl
	33	7	35.0	10	1	US-09-508-753B-195	Sequence 195, App
c	34	7	35.0	10	1	US-09-508-753B-289	Sequence 289, App
c	35	7	35.0	21	1	US-08-899-324-24	Sequence 24, Appl
c	36	7	35.0	21	1	US-08-329-892B-24	Sequence 24, Appl
c	37	7	35.0	37	1	US-08-874-569B-13	Sequence 13, Appl
c	38	7	35.0	37	1	US-09-955-518-13	Sequence 13, Appl
c	39	7	35.0	49	1	US-08-874-569B-4	Sequence 4, Appli
c	40	7	35.0	49	1	US-09-955-518-4	Sequence 4, Appli
c	41	6.8	34.0	10	1	US-09-508-753B-53	Sequence 53, Appl
	42	6.8	34.0	10	1	US-09-508-753B-94	Sequence 94, Appl
c	43	6.8	34.0	10	1	US-09-508-753B-460	Sequence 460, App
	44	6.6	33.0	21	1	US-08-874-569B-9	Sequence 9, Appli
	45	6.6	33.0	21	1	US-09-955-518-9	Sequence 9, Appli
c	46	6.4	32.0	8	1	US-08-859-954-130	Sequence 130, App
	47	6.4	32.0	8	1	US-08-859-954-131	Sequence 131, App
c	48	6.4	32.0	8	1	US-08-859-954-270	Sequence 270, App
c	49	6.4	32.0	8	1	US-08-859-954-509	Sequence 509, App
c	50	6.4	32.0	8	1	US-08-859-954-537	Sequence 537, App

ALIGNMENTS

```
RESULT 1
US-07-704-288C-25/c
; Sequence 25, Application US/07704288C
; Patent No. 5399680
;  GENERAL INFORMATION:
;    APPLICANT:  LAMB, CHRISTOPHER J.
;    APPLICANT:  ZHU, QUN
;    TITLE OF INVENTION:  PLANT DEFENSE GENES AND PLANT DEFENSE REGULATORY
;    TITLE OF INVENTION:  ELEMENTS
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
;      STREET:  444 South Flower Street, Suite 2000
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  90071-2921
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/704,288C
;      FILING DATE:  22-MAY-1991
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Reiter, Stephen E.
;      REGISTRATION NUMBER:  31,192
;      REFERENCE/DOCKET NUMBER:  P31 8899
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 546-4737
;      TELEFAX:  (619) 546-9392
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-07-704-288C-25

  Query Match           50.0%;  Score 10;  DB 1;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 1.6;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3322 AGGGGTTCCA 3331
              ||||||||||
```

```
Db         10 AGGGGTTCCA 1


RESULT 2
US-08-379-259-25/c
; Sequence 25, Application US/08379259
; Patent No. 5695939
;  GENERAL INFORMATION:
;    APPLICANT:  LAMB, CHRISTOPHER J.
;    APPLICANT:  ZHU, QUN
;    TITLE OF INVENTION:  PLANT DEFENSE GENES AND PLANT
;    TITLE OF INVENTION:  DEFENSE REGULATORY
;    TITLE OF INVENTION:  ELEMENTS
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
;      STREET:  444 South Flower Street, Suite 2000
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  90071-2921
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/379,259
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/704,288
;      FILING DATE:  22-MAY-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Reiter, Stephen E.
;      REGISTRATION NUMBER:  31,192
;      REFERENCE/DOCKET NUMBER:  P31 8899
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 546-4737
;      TELEFAX:  (619) 546-9392
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-379-259-25

  Query Match             50.0%;  Score 10;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.6;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3322 AGGGGTTCCA 3331
             ||||||||||
Db         10 AGGGGTTCCA 1


RESULT 3
US-08-874-569B-11/c
; Sequence 11, Application US/08874569B
; Patent No. 6306650
; GENERAL INFORMATION:
;  APPLICANT: Townes, Tim M.
;  APPLICANT:  Donze, David
;  TITLE OF INVENTION: DELTA-ERYTHROID KRUPPEL-LIKE FACTORS AND
;  TITLE OF INVENTION:  METHODS OF USE
;  FILE REFERENCE: 05118.0008U2
;  CURRENT APPLICATION NUMBER: US/08/874,569B
;  CURRENT FILING DATE:  1997-06-13
;  PRIOR APPLICATION NUMBER: 60/019,769
;  PRIOR FILING DATE: 1996-06-14
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;    LENGTH: 37
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence:\ No. 6306650e =
;    OTHER INFORMATION: synthetic construct
US-08-874-569B-11

  Query Match             43.0%;  Score 8.6;  DB 1;  Length 37;
  Best Local Similarity   73.3%;  Pred. No. 10;
  Matches   11;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3314 AGGGATTCAGGGGTT 3328
              ||||  ||||   |||
Db         20 AGGGTTTCATTAGTT 6


RESULT 4
US-09-955-518-11/c
; Sequence 11, Application US/09955518
; Patent No. 6475740
; GENERAL INFORMATION:
;  APPLICANT: Townes, Tim M.
;  APPLICANT:  Donze, David
;  TITLE OF INVENTION: DELTA-ERYTHROID KRUPPEL-LIKE FACTORS AND
;  TITLE OF INVENTION:  METHODS OF USE
;  FILE REFERENCE: 05118.0008U2
;  CURRENT APPLICATION NUMBER: US/09/955,518
;  CURRENT FILING DATE:  2001-09-18
;  PRIOR APPLICATION NUMBER: 60/019,769
;  PRIOR FILING DATE: 1996-06-14
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;    LENGTH: 37
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence:\ No. 6475740e =
;    OTHER INFORMATION: synthetic construct
US-09-955-518-11

  Query Match             43.0%;  Score 8.6;  DB 1;  Length 37;
  Best Local Similarity   73.3%;  Pred. No. 10;
  Matches   11;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3314 AGGGATTCAGGGGTT 3328
              ||||  ||||   |||
Db         20 AGGGTTTCATTAGTT 6


RESULT 5
US-09-508-753B-123
; Sequence 123, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
;  APPLICANT: Akira SHIMAMOTO
;  APPLICANT:  Yasuhiro FURUICHI
;  APPLICANT:  Yuko SHIBATA
;  APPLICANT:  Hiroko FUNAKI
;  APPLICANT:  Eiji OHARA
;  APPLICANT:  Masanori WATAHIKI
;  TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
;  FILE REFERENCE: 00162/HG
;  CURRENT APPLICATION NUMBER: US/09/508,753B
;  CURRENT FILING DATE:  2000-06-16
;  PRIOR APPLICATION NUMBER: JP 9/270324
;  PRIOR FILING DATE: 1997-09-18
```

```
;  NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 123
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-123

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 11;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3317 GATTCAGGGG 3326
              ||||||| ||
Db          1 GATTCAGAGG 10


RESULT 6
US-09-508-753B-149/c
; Sequence 149, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
;  APPLICANT: Akira SHIMAMOTO
;  APPLICANT:  Yasuhiro FURUICHI
;  APPLICANT:  Yuko SHIBATA
;  APPLICANT:  Hiroko FUNAKI
;  APPLICANT:  Eiji OHARA
;  APPLICANT:  Masanori WATAHIKI
;  TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
;  FILE REFERENCE: 00162/HG
;  CURRENT APPLICATION NUMBER: US/09/508,753B
;  CURRENT FILING DATE:  2000-06-16
;  PRIOR APPLICATION NUMBER: JP 9/270324
;  PRIOR FILING DATE: 1997-09-18
;  NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 149
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-149

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 11;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3317 GATTCAGGGG 3326
              ||||||| ||
Db         10 GATTCAGAGG 1


RESULT 7
US-08-899-324-21
; Sequence 21, Application US/08899324
; Patent No. 5945329
;  GENERAL INFORMATION:
;    APPLICANT:  Breddam, Klaus
;    APPLICANT:  Keilland-Brandt, Morten
;    APPLICANT:  Mortensen, Uffe
;    APPLICANT:  Olesen, Kjeld
;    APPLICANT:  Stennicke, Henning
;    APPLICANT:  Wagner, Fred
;    TITLE OF INVENTION:  CUSTOMIZED PROTEASES
;    NUMBER OF SEQUENCES:  33
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Merchant, Gould, Smith, Edell, Welter & Schmidt
;      STREET:  3100 No. 5945329west Center, 90 S. 7th Street
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  U.S.A.
;      ZIP:  55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/899,324
;      FILING DATE:  23-JUL-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/329,892
;      FILING DATE:  27-OCT-1994
;      APPLICATION NUMBER:  08/144,704
;      FILING DATE:  28-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kettleberger, Denise M
;      REGISTRATION NUMBER:  33,924
;      REFERENCE/DOCKET NUMBER:  8648.44USC1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612/332-5300
;      TELEFAX:  612/332-9081
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  30 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
;    IMMEDIATE SOURCE:
;      CLONE:  Oligo N51Q
US-08-899-324-21

  Query Match             41.0%;  Score 8.2;  DB 1;  Length 30;
  Best Local Similarity   76.9%;  Pred. No. 16;
  Matches   10;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3316 GGATTCAGGGGTT 3328
              || | |||||| |
Db         18 GGTTGCAGGGGGT 30


RESULT 8
US-08-329-892B-21
; Sequence 21, Application US/08329892B
; Patent No. 6187579
;  GENERAL INFORMATION:
;    APPLICANT:  Breddam, Klaus
;    APPLICANT:  Keilland-Brandt, Morten
;    APPLICANT:  Mortensen, Uffe
;    APPLICANT:  Olesen, Kjeld
;    APPLICANT:  Stennicke, Henning
;    APPLICANT:  Wagner, Fred
;    TITLE OF INVENTION:  CUSTOMIZED PROTEASE
;    NUMBER OF SEQUENCES:  33
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Merchant, Gould, Smith, Edell, Welter & Schmidt
;      STREET:  3100 No. 6187579west Center, 90 S. 7th Street
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  U.S.A.
;      ZIP:  55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/329,892B
```

```
;       FILING DATE:  27-OCT-1994
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/144,704
;       FILING DATE:  28-OCT-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Kettleberger, Denise M
;       REGISTRATION NUMBER:
;       REFERENCE/DOCKET NUMBER:  8648.44US01
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  612/332-5300
;       TELEFAX:  612/332-9081
;       TELEX:
;   INFORMATION FOR SEQ ID NO:  21:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  30 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  Genomic DNA
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     FRAGMENT TYPE:
;     ORIGINAL SOURCE:
;     IMMEDIATE SOURCE:
;       CLONE:  Oligo N51Q
US-08-329-892B-21

  Query Match             41.0%;  Score 8.2;  DB 1;  Length 30;
  Best Local Similarity   76.9%;  Pred. No. 16;
  Matches   10;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3316 GGATTCAGGGGTT 3328
              || | ||||||  |
Db         18 GGTTGCAGGGGGT 30


RESULT 9
US-08-859-954-239/c
; Sequence 239, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;     APPLICANT:  Hardin, Susan H.
;     APPLICANT:  Homayouni, Ramin
;     APPLICANT:  Hardin, Paul E.
;     TITLE OF INVENTION:  Design and Optimized Primer Library for
;     TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;     NUMBER OF SEQUENCES:  566
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Fulbright & Jaworski L.L.P.
;       STREET:  1301 McKinney, Suite 5100
;       CITY:  Houston
;       STATE:  Texas
;       COUNTRY:  U.S.A.
;       ZIP:  77010-3095
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/859,954
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/632,782
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Paul, Thomas D.
;       REGISTRATION NUMBER:  32,714
;       REFERENCE/DOCKET NUMBER:  D-5900
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  713/651-5325
;       TELEFAX:  713/651-5246
;   INFORMATION FOR SEQ ID NO:  239:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  8 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  other nucleic acid
;       DESCRIPTION:  /desc = "oligonucleotide"
;     HYPOTHETICAL:  YES
;     ANTI-SENSE:  YES
US-08-859-954-239

  Query Match             40.0%;  Score 8;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 5.1e+03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3314 AGGGATTC 3321
              ||||||||
Db          8 AGGGATTC 1


RESULT 10
US-08-590-804-20
; Sequence 20, Application US/08590804
; Patent No. 5780273
;  GENERAL INFORMATION:
;     APPLICANT:  Burg, J. Lawrence
;     TITLE OF INVENTION:  INSERTION ELEMENTS AND AMPLIFIABLE
;     TITLE OF INVENTION:  NUCLEIC ACIDS
;     NUMBER OF SEQUENCES:  32
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Amoco Corporation
;       STREET:  55 Shuman Blvd., Suite 600
;       CITY:  Naperville
;       STATE:  Illinois
;       COUNTRY:  USA
;       ZIP:  60563
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/590,804
;       FILING DATE:  24-JAN-1996
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/357,779
;       FILING DATE:
;       APPLICATION NUMBER:  US 08/045,587
;       FILING DATE:  09-APR-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Galloway, No. 5780273val B
;       REGISTRATION NUMBER:  33,595
;       REFERENCE/DOCKET NUMBER:  32,468
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  708-717-2447
;       TELEFAX:  708-717-2430
;   INFORMATION FOR SEQ ID NO:  20:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  10 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
US-08-590-804-20

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 17;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy       3321 CAGGGGTT 3328
             ||||||||
Db          1 CAGGGGTT 8


RESULT 11
US-09-508-753B-199
; Sequence 199, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
;  APPLICANT: Akira SHIMAMOTO
;  APPLICANT:  Yasuhiro FURUICHI
;  APPLICANT:  Yuko SHIBATA
;  APPLICANT:  Hiroko FUNAKI
;  APPLICANT:  Eiji OHARA
;  APPLICANT:  Masanori WATAHIKI
;  TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
;  FILE REFERENCE: 00162/HG
;  CURRENT APPLICATION NUMBER: US/09/508,753B
;  CURRENT FILING DATE:  2000-06-16
;  PRIOR APPLICATION NUMBER: JP 9/270324
;  PRIOR FILING DATE: 1997-09-18
;  NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 199
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-199

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 17;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3317 GATTCAGG 3324
             ||||||||
Db          3 GATTCAGG 10


RESULT 12
US-09-508-753B-253/c
; Sequence 253, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
;  APPLICANT: Akira SHIMAMOTO
;  APPLICANT:  Yasuhiro FURUICHI
;  APPLICANT:  Yuko SHIBATA
;  APPLICANT:  Hiroko FUNAKI
;  APPLICANT:  Eiji OHARA
;  APPLICANT:  Masanori WATAHIKI
;  TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
;  FILE REFERENCE: 00162/HG
;  CURRENT APPLICATION NUMBER: US/09/508,753B
;  CURRENT FILING DATE:  2000-06-16
;  PRIOR APPLICATION NUMBER: JP 9/270324
;  PRIOR FILING DATE: 1997-09-18
;  NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 253
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-253

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 17;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3317 GATTCAGG 3324
             ||||||||
Db          8 GATTCAGG 1


RESULT 13
US-08-899-324-6/c
; Sequence 6, Application US/08899324
; Patent No. 5945329
;  GENERAL INFORMATION:
;    APPLICANT:  Breddam, Klaus
;    APPLICANT:  Keilland-Brandt, Morten
;    APPLICANT:  Mortensen, Uffe
;    APPLICANT:  Olesen, Kjeld
;    APPLICANT:  Stennicke, Henning
;    APPLICANT:  Wagner, Fred
;    TITLE OF INVENTION:  CUSTOMIZED PROTEASES
;    NUMBER OF SEQUENCES:  33
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Merchant, Gould, Smith, Edell, Welter & Schmidt
;      STREET:  3100 No. 5945329west Center, 90 S. 7th Street
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  U.S.A.
;      ZIP:  55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/899,324
;      FILING DATE:  23-JUL-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/329,892
;      FILING DATE:  27-OCT-1994
;      APPLICATION NUMBER:  08/144,704
;      FILING DATE:  28-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kettleberger, Denise M
;      REGISTRATION NUMBER:  33,924
;      REFERENCE/DOCKET NUMBER:  8648.44USC1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612/332-5300
;      TELEFAX:  612/332-9081
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
US-08-899-324-6

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 4.5e+03;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3314 AGGGATTCA 3322
             ||| |||||
Db          9 AGGAATTCA 1


RESULT 14
US-08-329-892B-6/c
; Sequence 6, Application US/08329892B
; Patent No. 6187579
;  GENERAL INFORMATION:
;    APPLICANT:  Breddam, Klaus
;    APPLICANT:  Keilland-Brandt, Morten
```

```
;    APPLICANT:  Mortensen, Uffe
;    APPLICANT:  Olesen, Kjeld
;    APPLICANT:  Stennicke, Henning
;    APPLICANT:  Wagner, Fred
;    TITLE OF INVENTION:  CUSTOMIZED PROTEASE
;    NUMBER OF SEQUENCES:  33
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Merchant, Gould, Smith, Edell, Welter & Schmidt
;      STREET:  3100 No. 6187579west Center, 90 S. 7th Street
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  U.S.A.
;      ZIP:  55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/329,892B
;      FILING DATE:  27-OCT-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/144,704
;      FILING DATE:  28-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kettleberger, Denise M
;      REGISTRATION NUMBER:
;      REFERENCE/DOCKET NUMBER:  8648.44US01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612/332-5300
;      TELEFAX:  612/332-9081
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
US-08-329-892B-6

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 4.5e+03;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3314 AGGGATTCA 3322
              ||| |||||
Db          9 AGGAATTCA 1


RESULT 15
US-08-874-569B-18/c
; Sequence 18, Application US/08874569B
; Patent No. 6306650
; GENERAL INFORMATION:
;  APPLICANT: Townes, Tim M.
;  APPLICANT:  Donze, David
;  TITLE OF INVENTION: DELTA-ERYTHROID KRUPPEL-LIKE FACTORS AND
;  TITLE OF INVENTION:  METHODS OF USE
;  FILE REFERENCE: 05118.0008U2
;  CURRENT APPLICATION NUMBER: US/08/874,569B
;  CURRENT FILING DATE:  1997-06-13
;  PRIOR APPLICATION NUMBER: 60/019,769
;  PRIOR FILING DATE: 1996-06-14
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:\ No. 6306650e =
;   OTHER INFORMATION: synthetic construct
US-08-874-569B-18

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 4.5e+03;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3314 AGGGATTCA 3322
              |||| ||||
Db          9 AGGGTTTCA 1


RESULT 16
US-09-955-518-18/c
; Sequence 18, Application US/09955518
; Patent No. 6475740
; GENERAL INFORMATION:
;  APPLICANT: Townes, Tim M.
;  APPLICANT:  Donze, David
;  TITLE OF INVENTION: DELTA-ERYTHROID KRUPPEL-LIKE FACTORS AND
;  TITLE OF INVENTION:  METHODS OF USE
;  FILE REFERENCE: 05118.0008U2
;  CURRENT APPLICATION NUMBER: US/09/955,518
;  CURRENT FILING DATE:  2001-09-18
;  PRIOR APPLICATION NUMBER: 60/019,769
;  PRIOR FILING DATE: 1996-06-14
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:\ No. 6475740e =
;   OTHER INFORMATION: synthetic construct
US-09-955-518-18

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 4.5e+03;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3314 AGGGATTCA 3322
              |||| ||||
Db          9 AGGGTTTCA 1


RESULT 17
US-07-704-288C-5/c
; Sequence 5, Application US/07704288C
; Patent No. 5399680
;  GENERAL INFORMATION:
;    APPLICANT:  LAMB, CHRISTOPHER J.
;    APPLICANT:  ZHU, QUN
;    TITLE OF INVENTION:  PLANT DEFENSE GENES AND PLANT DEFENSE REGULATORY
;    TITLE OF INVENTION:  ELEMENTS
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
;      STREET:  444 South Flower Street, Suite 2000
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  90071-2921
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
```

```
;      APPLICATION NUMBER:  US/07/704,288C
;      FILING DATE:  22-MAY-1991
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Reiter, Stephen E.
;      REGISTRATION NUMBER:  31,192
;      REFERENCE/DOCKET NUMBER:  P31 8899
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 546-4737
;      TELEFAX:  (619) 546-9392
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
US-07-704-288C-5

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3317 GATTCAGGG 3325
              |||| ||||
Db          9 GATTGAGGG 1


RESULT 18
US-08-379-259-5/c
; Sequence 5, Application US/08379259
; Patent No. 5695939
;  GENERAL INFORMATION:
;    APPLICANT:  LAMB, CHRISTOPHER J.
;    APPLICANT:  ZHU, QUN
;    TITLE OF INVENTION:  PLANT DEFENSE GENES AND PLANT
;    TITLE OF INVENTION:  DEFENSE REGULATORY
;    TITLE OF INVENTION:  ELEMENTS
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
;      STREET:  444 South Flower Street, Suite 2000
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  90071-2921
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/379,259
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/704,288
;      FILING DATE:  22-MAY-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Reiter, Stephen E.
;      REGISTRATION NUMBER:  31,192
;      REFERENCE/DOCKET NUMBER:  P31 8899
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 546-4737
;      TELEFAX:  (619) 546-9392
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
US-08-379-259-5

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3317 GATTCAGGG 3325
              |||| ||||
Db          9 GATTGAGGG 1


RESULT 19
US-09-508-753B-87
; Sequence 87, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
;  APPLICANT: Akira SHIMAMOTO
;  APPLICANT:  Yasuhiro FURUICHI
;  APPLICANT:  Yuko SHIBATA
;  APPLICANT:  Hiroko FUNAKI
;  APPLICANT:  Eiji OHARA
;  APPLICANT:  Masanori WATAHIKI
;  TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
;  FILE REFERENCE: 00162/HG
;  CURRENT APPLICATION NUMBER: US/09/508,753B
;  CURRENT FILING DATE:  2000-06-16
;  PRIOR APPLICATION NUMBER: JP 9/270324
;  PRIOR FILING DATE: 1997-09-18
;  NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 87
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-87

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3319 TTCAGGGGT 3327
              ||||| |||
Db          1 TTCAGAGGT 9


RESULT 20
US-09-508-753B-121
; Sequence 121, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
;  APPLICANT: Akira SHIMAMOTO
;  APPLICANT:  Yasuhiro FURUICHI
;  APPLICANT:  Yuko SHIBATA
;  APPLICANT:  Hiroko FUNAKI
;  APPLICANT:  Eiji OHARA
;  APPLICANT:  Masanori WATAHIKI
;  TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
;  FILE REFERENCE: 00162/HG
;  CURRENT APPLICATION NUMBER: US/09/508,753B
;  CURRENT FILING DATE:  2000-06-16
;  PRIOR APPLICATION NUMBER: JP 9/270324
;  PRIOR FILING DATE: 1997-09-18
;  NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 121
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-121
```

```
  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3317 GATTCAGGG 3325
              ||||||| |
Db          1 GATTCAGAG 9


RESULT 21
US-09-508-753B-134/c
; Sequence 134, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
;  APPLICANT: Akira SHIMAMOTO
;  APPLICANT:  Yasuhiro FURUICHI
;  APPLICANT:  Yuko SHIBATA
;  APPLICANT:  Hiroko FUNAKI
;  APPLICANT:  Eiji OHARA
;  APPLICANT:  Masanori WATAHIKI
;  TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
;  FILE REFERENCE: 00162/HG
;  CURRENT APPLICATION NUMBER: US/09/508,753B
;  CURRENT FILING DATE:  2000-06-16
;  PRIOR APPLICATION NUMBER: JP 9/270324
;  PRIOR FILING DATE: 1997-09-18
;  NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 134
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-134

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3317 GATTCAGGG 3325
              ||||||| |
Db         10 GATTCAGAG 2


RESULT 22
US-09-508-753B-172
; Sequence 172, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
;  APPLICANT: Akira SHIMAMOTO
;  APPLICANT:  Yasuhiro FURUICHI
;  APPLICANT:  Yuko SHIBATA
;  APPLICANT:  Hiroko FUNAKI
;  APPLICANT:  Eiji OHARA
;  APPLICANT:  Masanori WATAHIKI
;  TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
;  FILE REFERENCE: 00162/HG
;  CURRENT APPLICATION NUMBER: US/09/508,753B
;  CURRENT FILING DATE:  2000-06-16
;  PRIOR APPLICATION NUMBER: JP 9/270324
;  PRIOR FILING DATE: 1997-09-18
;  NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 172
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-172

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3321 CAGGGGTTC 3329
              ||| |||||
Db          2 CAGAGGTTC 10


RESULT 23
US-09-508-753B-15/c
; Sequence 15, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
;  APPLICANT: Akira SHIMAMOTO
;  APPLICANT:  Yasuhiro FURUICHI
;  APPLICANT:  Yuko SHIBATA
;  APPLICANT:  Hiroko FUNAKI
;  APPLICANT:  Eiji OHARA
;  APPLICANT:  Masanori WATAHIKI
;  TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
;  FILE REFERENCE: 00162/HG
;  CURRENT APPLICATION NUMBER: US/09/508,753B
;  CURRENT FILING DATE:  2000-06-16
;  PRIOR APPLICATION NUMBER: JP 9/270324
;  PRIOR FILING DATE: 1997-09-18
;  NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 15
;   LENGTH: 37
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Oligoribonucleotide
US-09-508-753B-15

  Query Match             36.0%;  Score 7.2;  DB 1;  Length 37;
  Best Local Similarity   75.0%;  Pred. No. 54;
  Matches    9;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3320 TCAGGGGTTCCA 3331
              ||||| || | |
Db         24 TCAGGAGTCCTA 13


RESULT 24
US-08-859-954-32
; Sequence 32, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
```

```
;       REGISTRATION NUMBER:  32,714
;       REFERENCE/DOCKET NUMBER:  D-5900
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  713/651-5325
;       TELEFAX:  713/651-5246
;   INFORMATION FOR SEQ ID NO:  32:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  8 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  other nucleic acid
;       DESCRIPTION:  /desc = "oligonucleotide"
;     HYPOTHETICAL:  YES
;     ANTI-SENSE:  YES
US-08-859-954-32

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 5.1e+03;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3325 GGTTCCA 3331
             |||||||
Db          1 GGTTCCA 7


RESULT 25
US-08-859-954-240/c
; Sequence 240, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  240:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-240

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 5.1e+03;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3315 GGGATTC 3321
             |||||||
Db          7 GGGATTC 1


RESULT 26
US-08-859-954-292/c
; Sequence 292, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  292:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-292

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 5.1e+03;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3326 GTTCCAG 3332
             |||||||
Db          7 GTTCCAG 1


RESULT 27
US-09-063-450-8/c
; Sequence 8, Application US/09063450
; Patent No. 6109776
```

```
; GENERAL INFORMATION:
;  APPLICANT: Gene Logic, Inc.
;  TITLE OF INVENTION: Method and System for Computationally Identifying
;  TITLE OF INVENTION: Clusters Within a Set of Sequences
;  FILE REFERENCE: 77001.002
;  CURRENT APPLICATION NUMBER: US/09/063,450
;  CURRENT FILING DATE: 1998-04-21
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 8
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:example
;   OTHER INFORMATION: sequence illustrating a computational methodology
US-09-063-450-8

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 5.1e+03;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3314 AGGGATT 3320
             |||||||
Db          7 AGGGATT 1


RESULT 28
US-09-398-499-15/c
; Sequence 15, Application US/09398499
; Patent No. 6284466
; GENERAL INFORMATION:
;  APPLICANT:  Benson, Andrew K.
;  TITLE OF INVENTION:  HIGH RESOLUTION GENOME SCANNING
;  FILE REFERENCE:  UNL 2963
;  CURRENT APPLICATION NUMBER: US/09/398,499
;  CURRENT FILING DATE:  1999-09-17
;  PRIOR APPLICATION NUMBER:  60/101,011
;  PRIOR FILING DATE:  1998-09-18
;  NUMBER OF SEQ ID NOS:  58
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 15
;   LENGTH: 8
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Primer
US-09-398-499-15

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 5.1e+03;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3327 TTCCAGC 3333
             |||||||
Db          7 TTCCAGC 1


RESULT 29
US-09-398-499-38
; Sequence 38, Application US/09398499
; Patent No. 6284466
; GENERAL INFORMATION:
;  APPLICANT:  Benson, Andrew K.
;  TITLE OF INVENTION:  HIGH RESOLUTION GENOME SCANNING
;  FILE REFERENCE:  UNL 2963
;  CURRENT APPLICATION NUMBER: US/09/398,499
;  CURRENT FILING DATE:  1999-09-17
;  PRIOR APPLICATION NUMBER:  60/101,011
;  PRIOR FILING DATE:  1998-09-18
;  NUMBER OF SEQ ID NOS:  58
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 38
;   LENGTH: 8
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Primer
US-09-398-499-38

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 5.1e+03;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3327 TTCCAGC 3333
             |||||||
Db          2 TTCCAGC 8


RESULT 30
US-08-590-804-25/c
; Sequence 25, Application US/08590804
; Patent No. 5780273
;  GENERAL INFORMATION:
;    APPLICANT:  Burg, J. Lawrence
;    TITLE OF INVENTION:  INSERTION ELEMENTS AND AMPLIFIABLE
;    TITLE OF INVENTION:  NUCLEIC ACIDS
;    NUMBER OF SEQUENCES:  32
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amoco Corporation
;      STREET:  55 Shuman Blvd., Suite 600
;      CITY:  Naperville
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60563
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/590,804
;      FILING DATE:  24-JAN-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/357,779
;      FILING DATE:
;      APPLICATION NUMBER:  US 08/045,587
;      FILING DATE:  09-APR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Galloway, No. 5780273val B
;      REGISTRATION NUMBER:  33,595
;      REFERENCE/DOCKET NUMBER:  32,468
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  708-717-2447
;      TELEFAX:  708-717-2430
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-590-804-25

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 56;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3317 GATTCAG 3323
             |||||||
Db          7 GATTCAG 1


RESULT 31
```

```
US-09-398-499-58
; Sequence 58, Application US/09398499
; Patent No. 6284466
; GENERAL INFORMATION:
;  APPLICANT:  Benson, Andrew K.
;  TITLE OF INVENTION:  HIGH RESOLUTION GENOME SCANNING
;  FILE REFERENCE:  UNL 2963
;  CURRENT APPLICATION NUMBER: US/09/398,499
;  CURRENT FILING DATE:  1999-09-17
;  PRIOR APPLICATION NUMBER:  60/101,011
;  PRIOR FILING DATE:  1998-09-18
;  NUMBER OF SEQ ID NOS:  58
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 58
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Primer
US-09-398-499-58

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 56;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3327 TTCCAGC 3333
             |||||||
Db          4 TTCCAGC 10


RESULT 32
US-09-508-753B-22/c
; Sequence 22, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
;  APPLICANT: Akira SHIMAMOTO
;  APPLICANT:  Yasuhiro FURUICHI
;  APPLICANT:  Yuko SHIBATA
;  APPLICANT:  Hiroko FUNAKI
;  APPLICANT:  Eiji OHARA
;  APPLICANT:  Masanori WATAHIKI
;  TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
;  FILE REFERENCE: 00162/HG
;  CURRENT APPLICATION NUMBER: US/09/508,753B
;  CURRENT FILING DATE:  2000-06-16
;  PRIOR APPLICATION NUMBER: JP 9/270324
;  PRIOR FILING DATE: 1997-09-18
;  NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 22
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-22

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 56;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3327 TTCCAGC 3333
             |||||||
Db          8 TTCCAGC 2


RESULT 33
US-09-508-753B-195
; Sequence 195, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
;  APPLICANT: Akira SHIMAMOTO
;  APPLICANT:  Yasuhiro FURUICHI
;  APPLICANT:  Yuko SHIBATA
;  APPLICANT:  Hiroko FUNAKI
;  APPLICANT:  Eiji OHARA
;  APPLICANT:  Masanori WATAHIKI
;  TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
;  FILE REFERENCE: 00162/HG
;  CURRENT APPLICATION NUMBER: US/09/508,753B
;  CURRENT FILING DATE:  2000-06-16
;  PRIOR APPLICATION NUMBER: JP 9/270324
;  PRIOR FILING DATE: 1997-09-18
;  NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 195
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-195

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 56;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3316 GGATTCA 3322
             |||||||
Db          1 GGATTCA 7


RESULT 34
US-09-508-753B-289/c
; Sequence 289, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
;  APPLICANT: Akira SHIMAMOTO
;  APPLICANT:  Yasuhiro FURUICHI
;  APPLICANT:  Yuko SHIBATA
;  APPLICANT:  Hiroko FUNAKI
;  APPLICANT:  Eiji OHARA
;  APPLICANT:  Masanori WATAHIKI
;  TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
;  FILE REFERENCE: 00162/HG
;  CURRENT APPLICATION NUMBER: US/09/508,753B
;  CURRENT FILING DATE:  2000-06-16
;  PRIOR APPLICATION NUMBER: JP 9/270324
;  PRIOR FILING DATE: 1997-09-18
;  NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 289
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-289

  Query Match             35.0%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 56;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3316 GGATTCA 3322
             |||||||
Db         10 GGATTCA 4


RESULT 35
US-08-899-324-24/c
; Sequence 24, Application US/08899324
; Patent No. 5945329
;  GENERAL INFORMATION:
;    APPLICANT:  Breddam, Klaus
;    APPLICANT:  Keilland-Brandt, Morten
;    APPLICANT:  Mortensen, Uffe
;    APPLICANT:  Olesen, Kjeld
;    APPLICANT:  Stennicke, Henning
;    APPLICANT:  Wagner, Fred
```

```
;    TITLE OF INVENTION:  CUSTOMIZED PROTEASES
;    NUMBER OF SEQUENCES:  33
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Merchant, Gould, Smith, Edell, Welter & Schmidt
;      STREET:  3100 No. 5945329west Center, 90 S. 7th Street
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  U.S.A.
;      ZIP:  55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/899,324
;      FILING DATE:  23-JUL-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/329,892
;      FILING DATE:  27-OCT-1994
;      APPLICATION NUMBER:  08/144,704
;      FILING DATE:  28-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kettleberger, Denise M
;      REGISTRATION NUMBER:  33,924
;      REFERENCE/DOCKET NUMBER:  8648.44USC1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612/332-5300
;      TELEFAX:  612/332-9081
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
;    IMMEDIATE SOURCE:
;      CLONE:  Oligo E145D
US-08-899-324-24

  Query Match             35.0%;  Score 7;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 63;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3315 GGGATTC 3321
                 |||||||
Db         14 GGGATTC 8


RESULT 36
US-08-329-892B-24/c
; Sequence 24, Application US/08329892B
; Patent No. 6187579
;  GENERAL INFORMATION:
;    APPLICANT:  Breddam, Klaus
;    APPLICANT:  Keilland-Brandt, Morten
;    APPLICANT:  Mortensen, Uffe
;    APPLICANT:  Olesen, Kjeld
;    APPLICANT:  Stennicke, Henning
;    APPLICANT:  Wagner, Fred
;    TITLE OF INVENTION:  CUSTOMIZED PROTEASE
;    NUMBER OF SEQUENCES:  33
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Merchant, Gould, Smith, Edell, Welter & Schmidt
;      STREET:  3100 No. 6187579west Center, 90 S. 7th Street
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  U.S.A.
;      ZIP:  55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/329,892B
;      FILING DATE:  27-OCT-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/144,704
;      FILING DATE:  28-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kettleberger, Denise M
;      REGISTRATION NUMBER:
;      REFERENCE/DOCKET NUMBER:  8648.44US01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612/332-5300
;      TELEFAX:  612/332-9081
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
;    IMMEDIATE SOURCE:
;      CLONE:  Oligo E145D
US-08-329-892B-24

  Query Match             35.0%;  Score 7;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 63;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3315 GGGATTC 3321
                 |||||||
Db         14 GGGATTC 8


RESULT 37
US-08-874-569B-13/c
; Sequence 13, Application US/08874569B
; Patent No. 6306650
; GENERAL INFORMATION:
;  APPLICANT: Townes, Tim M.
;  APPLICANT:  Donze, David
;  TITLE OF INVENTION: DELTA-ERYTHROID KRUPPEL-LIKE FACTORS AND
;  TITLE OF INVENTION:  METHODS OF USE
;  FILE REFERENCE: 05118.0008U2
;  CURRENT APPLICATION NUMBER: US/08/874,569B
;  CURRENT FILING DATE:  1997-06-13
;  PRIOR APPLICATION NUMBER: 60/019,769
;  PRIOR FILING DATE: 1996-06-14
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
;   LENGTH: 37
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:\ No. 6306650e =
;   OTHER INFORMATION: synthetic construct
US-08-874-569B-13

  Query Match             35.0%;  Score 7;  DB 1;  Length 37;
  Best Local Similarity   66.7%;  Pred. No. 68;
```

```
  Matches   10;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       3314 AGGGATTCAGGGGTT 3328
              |||||    | ||||
Db         20 AGGGAGGGTGTGGTT 6


RESULT 38
US-09-955-518-13/c
; Sequence 13, Application US/09955518
; Patent No. 6475740
; GENERAL INFORMATION:
;  APPLICANT: Townes, Tim M.
;  APPLICANT:  Donze, David
;  TITLE OF INVENTION: DELTA-ERYTHROID KRUPPEL-LIKE FACTORS AND
;  TITLE OF INVENTION:  METHODS OF USE
;  FILE REFERENCE: 05118.0008U2
;  CURRENT APPLICATION NUMBER: US/09/955,518
;  CURRENT FILING DATE:  2001-09-18
;  PRIOR APPLICATION NUMBER: 60/019,769
;  PRIOR FILING DATE: 1996-06-14
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
;   LENGTH: 37
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:\ No. 6475740e =
;   OTHER INFORMATION: synthetic construct
US-09-955-518-13

  Query Match             35.0%;  Score 7;  DB 1;  Length 37;
  Best Local Similarity   66.7%;  Pred. No. 68;
  Matches   10;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       3314 AGGGATTCAGGGGTT 3328
              |||||    | ||||
Db         20 AGGGAGGGTGTGGTT 6


RESULT 39
US-08-874-569B-4/c
; Sequence 4, Application US/08874569B
; Patent No. 6306650
; GENERAL INFORMATION:
;  APPLICANT: Townes, Tim M.
;  APPLICANT:  Donze, David
;  TITLE OF INVENTION: DELTA-ERYTHROID KRUPPEL-LIKE FACTORS AND
;  TITLE OF INVENTION:  METHODS OF USE
;  FILE REFERENCE: 05118.0008U2
;  CURRENT APPLICATION NUMBER: US/08/874,569B
;  CURRENT FILING DATE:  1997-06-13
;  PRIOR APPLICATION NUMBER: 60/019,769
;  PRIOR FILING DATE: 1996-06-14
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 49
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:\ No. 6306650e =
;   OTHER INFORMATION: synthetic construct
US-08-874-569B-4

  Query Match             35.0%;  Score 7;  DB 1;  Length 49;
  Best Local Similarity   66.7%;  Pred. No. 70;
  Matches   10;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       3314 AGGGATTCAGGGGTT 3328
              |||||    | ||||
Db         33 AGGGAGGGTGTGGTT 19


RESULT 40
US-09-955-518-4/c
; Sequence 4, Application US/09955518
; Patent No. 6475740
; GENERAL INFORMATION:
;  APPLICANT: Townes, Tim M.
;  APPLICANT:  Donze, David
;  TITLE OF INVENTION: DELTA-ERYTHROID KRUPPEL-LIKE FACTORS AND
;  TITLE OF INVENTION:  METHODS OF USE
;  FILE REFERENCE: 05118.0008U2
;  CURRENT APPLICATION NUMBER: US/09/955,518
;  CURRENT FILING DATE:  2001-09-18
;  PRIOR APPLICATION NUMBER: 60/019,769
;  PRIOR FILING DATE: 1996-06-14
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 49
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:\ No. 6475740e =
;   OTHER INFORMATION: synthetic construct
US-09-955-518-4

  Query Match             35.0%;  Score 7;  DB 1;  Length 49;
  Best Local Similarity   66.7%;  Pred. No. 70;
  Matches   10;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       3314 AGGGATTCAGGGGTT 3328
              |||||    | ||||
Db         33 AGGGAGGGTGTGGTT 19


RESULT 41
US-09-508-753B-53/c
; Sequence 53, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
;  APPLICANT: Akira SHIMAMOTO
;  APPLICANT:  Yasuhiro FURUICHI
;  APPLICANT:  Yuko SHIBATA
;  APPLICANT:  Hiroko FUNAKI
;  APPLICANT:  Eiji OHARA
;  APPLICANT:  Masanori WATAHIKI
;  TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
;  FILE REFERENCE: 00162/HG
;  CURRENT APPLICATION NUMBER: US/09/508,753B
;  CURRENT FILING DATE:  2000-06-16
;  PRIOR APPLICATION NUMBER: JP 9/270324
;  PRIOR FILING DATE: 1997-09-18
;  NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 53
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-53

  Query Match             34.0%;  Score 6.8;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 71;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3317 GATTCAGGGG 3326
              | |||||| |
Db         10 GTTTCAGGAG 1


RESULT 42
US-09-508-753B-94
```

```
; Sequence 94, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
;  APPLICANT: Akira SHIMAMOTO
;  APPLICANT:  Yasuhiro FURUICHI
;  APPLICANT:  Yuko SHIBATA
;  APPLICANT:  Hiroko FUNAKI
;  APPLICANT:  Eiji OHARA
;  APPLICANT:  Masanori WATAHIKI
;  TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
;  FILE REFERENCE: 00162/HG
;  CURRENT APPLICATION NUMBER: US/09/508,753B
;  CURRENT FILING DATE:  2000-06-16
;  PRIOR APPLICATION NUMBER: JP 9/270324
;  PRIOR FILING DATE: 1997-09-18
;  NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 94
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-94

  Query Match             34.0%;  Score 6.8;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 71;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3317 GATTCAGGGG 3326
             | ||||||  |
Db          1 GTTTCAGGAG 10


RESULT 43
US-09-508-753B-460/c
; Sequence 460, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
;  APPLICANT: Akira SHIMAMOTO
;  APPLICANT:  Yasuhiro FURUICHI
;  APPLICANT:  Yuko SHIBATA
;  APPLICANT:  Hiroko FUNAKI
;  APPLICANT:  Eiji OHARA
;  APPLICANT:  Masanori WATAHIKI
;  TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
;  FILE REFERENCE: 00162/HG
;  CURRENT APPLICATION NUMBER: US/09/508,753B
;  CURRENT FILING DATE:  2000-06-16
;  PRIOR APPLICATION NUMBER: JP 9/270324
;  PRIOR FILING DATE: 1997-09-18
;  NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 460
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-460

  Query Match             34.0%;  Score 6.8;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 71;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3317 GATTCAGGGG 3326
             |||| | |||
Db         10 GATTTACGGG 1


RESULT 44
US-08-874-569B-9
; Sequence 9, Application US/08874569B
; Patent No. 6306650
; GENERAL INFORMATION:
;  APPLICANT: Townes, Tim M.
;  APPLICANT:  Donze, David
;  TITLE OF INVENTION: DELTA-ERYTHROID KRUPPEL-LIKE FACTORS AND
;  TITLE OF INVENTION:  METHODS OF USE
;  FILE REFERENCE: 05118.0008U2
;  CURRENT APPLICATION NUMBER: US/08/874,569B
;  CURRENT FILING DATE:  1997-06-13
;  PRIOR APPLICATION NUMBER: 60/019,769
;  PRIOR FILING DATE: 1996-06-14
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:\ No. 6306650e =
;   OTHER INFORMATION: synthetic construct
US-08-874-569B-9

  Query Match             33.0%;  Score 6.6;  DB 1;  Length 21;
  Best Local Similarity   69.2%;  Pred. No. 1e+02;
  Matches    9;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3319 TTCAGGGGTTCCA 3331
              |||   || ||||
Db          6 TTCTCAGGATCCA 18


RESULT 45
US-09-955-518-9
; Sequence 9, Application US/09955518
; Patent No. 6475740
; GENERAL INFORMATION:
;  APPLICANT: Townes, Tim M.
;  APPLICANT:  Donze, David
;  TITLE OF INVENTION: DELTA-ERYTHROID KRUPPEL-LIKE FACTORS AND
;  TITLE OF INVENTION:  METHODS OF USE
;  FILE REFERENCE: 05118.0008U2
;  CURRENT APPLICATION NUMBER: US/09/955,518
;  CURRENT FILING DATE:  2001-09-18
;  PRIOR APPLICATION NUMBER: 60/019,769
;  PRIOR FILING DATE: 1996-06-14
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:\ No. 6475740e =
;   OTHER INFORMATION: synthetic construct
US-09-955-518-9

  Query Match             33.0%;  Score 6.6;  DB 1;  Length 21;
  Best Local Similarity   69.2%;  Pred. No. 1e+02;
  Matches    9;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3319 TTCAGGGGTTCCA 3331
              |||   || ||||
Db          6 TTCTCAGGATCCA 18


RESULT 46
US-08-859-954-130/c
; Sequence 130, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
```

```
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  130:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-130

  Query Match             32.0%;  Score 6.4;  DB 1;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 5.1e+03;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3314 AGGGATTC 3321
                |||||.||
Db             8 AGGGAATC 1


RESULT 47
US-08-859-954-131
; Sequence 131, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  131:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-131

  Query Match             32.0%;  Score 6.4;  DB 1;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 5.1e+03;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3325 GGTTCCAG 3332
                | ||||||
Db             1 GATTCCAG 8


RESULT 48
US-08-859-954-270/c
; Sequence 270, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  270:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
```

```
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-270

  Query Match             32.0%;  Score 6.4;  DB 1;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 5.1e+03;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3322 AGGGGTTC 3329
              ||| |||| 
Db          8 AGGAGTTC 1


RESULT 49
US-08-859-954-509/c
; Sequence 509, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  509:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-509

  Query Match             32.0%;  Score 6.4;  DB 1;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 5.1e+03;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3320 TCAGGGGT 3327
              ||||| || 
Db          8 TCAGGAGT 1


RESULT 50
US-08-859-954-537/c
; Sequence 537, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  537:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-537

  Query Match             32.0%;  Score 6.4;  DB 1;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 5.1e+03;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3320 TCAGGGGT 3327
              ||||| || 
Db          8 TCAGGTGT 1


Search completed: October 2, 2003, 15:40:43
Job time : 1 secs
```

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: October 2, 2003, 15:32:18 ; Search time 0.001 Seconds
(without alignments)
17.800 Million cell updates/sec

Title: us-09-676-436-3
Perfect score: 20
Sequence: 1 agggattcaggggttccagc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 42 seqs, 445 residues

Total number of hits satisfying chosen parameters: 84

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 42 summaries

Database : rge.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	12.4	62.0	14	1	a42556	TOIG of: a42556
	2	12.4	62.0	14	1	a88747	TOIG of: a88747
	3	12.4	62.0	14	1	bd066260	TOIG of: bd06626
c	4	11	55.0	11	1	ax471613	TOIG of: ax47161
c	5	11	55.0	11	1	ax628456	TOIG of: ax62845
c	6	10	50.0	10	1	i84475	TOIG of: i84475
c	7	10	50.0	11	1	ax626783	TOIG of: ax62678
c	8	9.4	47.0	11	1	ax470549	TOIG of: ax47054
c	9	9.4	47.0	11	1	ax623428	TOIG of: ax62342
	10	9.4	47.0	11	1	ax629578	TOIG of: ax62957
c	11	9.4	47.0	11	1	ax630849	TOIG of: ax63084
	12	9	45.0	10	1	e39766	TOIG of: e39766
	13	9	45.0	11	1	ax471317	TOIG of: ax47131
	14	9	45.0	11	1	ax624360	TOIG of: ax62436
	15	9	45.0	11	1	ax625683	TOIG of: ax62568
c	16	9	45.0	11	1	ax625706	TOIG of: ax62570
	17	9	45.0	11	1	ax626201	TOIG of: ax62620
	18	9	45.0	11	1	ax631781	TOIG of: ax63178
	19	8.4	42.0	10	1	ar303398	TOIG of: ar30339
c	20	8.4	42.0	10	1	ar303424	TOIG of: ar30342
c	21	8.4	42.0	10	1	ax112965	TOIG of: ax11296
	22	8.4	42.0	10	1	ax152520	TOIG of: ax15252
	23	8.4	42.0	10	1	ax153581	TOIG of: ax15358
	24	8.4	42.0	10	1	ax153631	TOIG of: ax15363
	25	8.4	42.0	10	1	ax301326	TOIG of: ax30132
	26	8.4	42.0	10	1	ax667821	TOIG of: ax66782
	27	8.4	42.0	10	1	ax667826	TOIG of: ax66782
	28	8.4	42.0	10	1	ax667888	TOIG of: ax66788
	29	8.4	42.0	10	1	bd007762	TOIG of: bd00776
c	30	8.4	42.0	10	1	bd007794	TOIG of: bd00779
	31	8.4	42.0	10	1	bd083142	TOIG of: bd08314
c	32	8.4	42.0	10	1	bd083204	TOIG of: bd08320
c	33	8.4	42.0	10	1	bd083268	TOIG of: bd08326
	34	8.4	42.0	10	1	e39536	TOIG of: e39536
	35	8.4	42.0	10	1	e54753	TOIG of: e54753
	36	8	40.0	10	1	ar017955	TOIG of: ar01795
	37	8	40.0	10	1	ar303474	TOIG of: ar30347
c	38	8	40.0	10	1	ar303528	TOIG of: ar30352
	39	8	40.0	10	1	ax152673	TOIG of: ax15267
	40	8	40.0	10	1	ax301451	TOIG of: ax30145
	41	8	40.0	10	1	ax301542	TOIG of: ax30154
	42	8	40.0	10	1	ax719148	TOIG of: ax71914

ALIGNMENTS

RESULT 1
a42556
; TOIG of: a42556 check: 7525 from: 1 to: 14
;
; LOCUS A42556 14 bp DNA linear PAT 06-MAR-1997
; DEFINITION Sequence 72 from Patent WO9502051.
; ACCESSION A42556
; VERSION A42556.1 GI:2298005
; KEYWORDS .
; SOURCE unidentified
; ORGANISM unidentified
; unclassified.
; REFERENCE 1 (bases 1 to 14)
; AUTHORS Schlingensiepen,G., Schlingensiepen,R., Schlingensiepen,K. and Brysch,W.
; TITLE A PHARMACEUTICAL COMPOSITION COMPRISING ANTISENSE-NUCLEIC ACID FOR PREVENTION AND/OR TREATMENT OF NEURONAL INJURY, DEGENERATION AND CELL DEATH AND FOR THE TREATMENT OF NEOPLASMS
; JOURNAL Patent: WO 9502051-A 72 19-JAN-1995;
; BIOGNOSTIK GES FUER BIOMOLEKUL (DE)
; COMMENT Other publication AU 7345694 950206.
; FEATURES Location/Qualifiers
; source 1. .14
; /organism="unidentified"
; /mol_type="genomic DNA"
; /db_xref="taxon:32644"
; BASE COUNT 3 a 4 c 3 g 4 t
; ORIGIN
;
; A42556 Length: 14 October 2, 2003 14:56 Type: N Check: 7525 ..
a42556

Query Match 62.0%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.3;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       3318 ATTCAGGGGTTCCA 3331
              ||||||| ||||||
Db             1 ATTCAGGCGTTCCA 14
```

RESULT 2
a88747
; TOIG of: a88747 check: 7525 from: 1 to: 14
;
; LOCUS A88747 14 bp DNA linear PAT 22-JAN-2000
; DEFINITION Sequence 895 from Patent WO9833904.
; ACCESSION A88747
; VERSION A88747.1 GI:6737317
; KEYWORDS .
; SOURCE unidentified
; ORGANISM unidentified
; unclassified.
; REFERENCE 1 (bases 1 to 14)
; AUTHORS Brysch,W. and Schlingensiepen,K.
; TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
; JOURNAL Patent: WO 9833904-A 895 06-AUG-1998;
; BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
; FEATURES Location/Qualifiers

```
;      source          1. .14
;                      /organism="unidentified"
;                      /mol_type="genomic DNA"
;                      /db_xref="taxon:32644"
; BASE COUNT        3 a      4 c      3 g      4 t
; ORIGIN
;
;   A88747  Length: 14  October 2, 2003 14:56  Type: N  Check: 7525  ..
a88747

  Query Match             62.0%;  Score 12.4;  DB 1;  Length 14;
  Best Local Similarity   92.9%;  Pred. No. 2.3;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3318 ATTCAGGGGTTCCA 3331
              ||||||| ||||||
Db          1 ATTCAGGCGTTCCA 14


RESULT 3
bd066260
;  TOIG of: bd066260  check: 7525  from: 1  to: 14
;
; LOCUS       BD066260                 14 bp    DNA     linear   PAT 27-AUG-2002
; DEFINITION  An antisense oligonucleotide preparation method.
; ACCESSION   BD066260
; VERSION     BD066260.1  GI:22611863
; KEYWORDS    JP 2001511000-A/895.
; SOURCE      unidentified
;   ORGANISM  unidentified
;             unclassified.
; REFERENCE   1  (bases 1 to 14)
;   AUTHORS   Schlingensiepen,K.H. and Brysch,W.
;   TITLE     An antisense oligonucleotide preparation method
;   JOURNAL   Patent: JP 2001511000-A 895 07-AUG-2001;
;             BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
; COMMENT     OS   Unknown
;             PN   JP 2001511000-A/895
;             PD   07-AUG-2001
;             PF   30-JAN-1998 JP 1998532533
;             PR   31-JAN-1997 EP   97101531.8
;             PI   KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
;             PC   C12N15/11,C07H21/04,A61K31/70
;             CC   An antisense oligonucleotide preparation method FH   Key
;                   Location/Qualifiers
;             FT   source          1. .14
;             FT                   /organism='Unknown'.
; FEATURES              Location/Qualifiers
;      source           1. .14
;                       /organism="unidentified"
;                       /mol_type="genomic DNA"
;                       /db_xref="taxon:32644"
; BASE COUNT        3 a      4 c      3 g      4 t
; ORIGIN
;
;  BD066260  Length: 14  October 2, 2003 14:56  Type: N  Check: 7525  ..
bd066260

  Query Match             62.0%;  Score 12.4;  DB 1;  Length 14;
  Best Local Similarity   92.9%;  Pred. No. 2.3;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3318 ATTCAGGGGTTCCA 3331
              ||||||| ||||||
Db          1 ATTCAGGCGTTCCA 14


RESULT 4
ax471613/c
;  TOIG of: ax471613  check: 4620  from: 1  to: 11
;
; LOCUS       AX471613                 11 bp    DNA     linear   PAT 09-AUG-2002
; DEFINITION  Sequence 1190 from Patent WO02053773.
; ACCESSION   AX471613
; VERSION     AX471613.1  GI:22206738
; KEYWORDS    .
; SOURCE      Homo sapiens (human)
;   ORGANISM  Homo sapiens
;             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
;             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
; REFERENCE   1
;   AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
;   TITLE     Method for determining skin stress or skin ageing in vitro
;   JOURNAL   Patent: WO 02053773-A 1190 11-JUL-2002;
;             HENKEL KGAA (DE)
; FEATURES              Location/Qualifiers
;      source           1. .11
;                       /organism="Homo sapiens"
;                       /mol_type="genomic DNA"
;                       /db_xref="taxon:9606"
; BASE COUNT        2 a      6 c      1 g      2 t
; ORIGIN
;
;  AX471613  Length: 11  October 2, 2003 14:56  Type: N  Check: 4620  ..
ax471613

  Query Match             55.0%;  Score 11;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 5.4;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3315 GGGATTCAGGG 3325
              ||||||||||
Db         11 GGGATTCAGGG 1


RESULT 5
ax628456/c
;  TOIG of: ax628456  check: 4620  from: 1  to: 11
;
; LOCUS       AX628456                 11 bp    DNA     linear   PAT 21-FEB-2003
; DEFINITION  Sequence 5497 from Patent WO02053774.
; ACCESSION   AX628456
; VERSION     AX628456.1  GI:28456494
; KEYWORDS    .
; SOURCE      Homo sapiens (human)
;   ORGANISM  Homo sapiens
;             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
;             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
; REFERENCE   1
;   AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
;   TITLE     Method for determining homeostasis of the skin
;   JOURNAL   Patent: WO 02053774-A 5497 11-JUL-2002;
;             Henkel Kommanditgesellschaft auf Aktien (DE)
; FEATURES              Location/Qualifiers
;      source           1. .11
;                       /organism="Homo sapiens"
;                       /mol_type="genomic DNA"
;                       /db_xref="taxon:9606"
; BASE COUNT        2 a      6 c      1 g      2 t
; ORIGIN
;
;  AX628456  Length: 11  October 2, 2003 14:56  Type: N  Check: 4620  ..
ax628456

  Query Match             55.0%;  Score 11;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 5.4;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3315 GGGATTCAGGG 3325
              ||||||||||
Db         11 GGGATTCAGGG 1


RESULT 6
i84475/c
;  TOIG of: i84475  check: 3874  from: 1  to: 10
```

```
;
; LOCUS       I84475                    10 bp    DNA     linear   PAT 04-APR-1998
; DEFINITION  Sequence 25 from patent US 5695939.
; ACCESSION   I84475
; VERSION     I84475.1  GI:3021995
; KEYWORDS    .
; SOURCE      Unknown.
;   ORGANISM  Unknown.
;             Unclassified.
; REFERENCE   1  (bases 1 to 10)
;   AUTHORS   Zhu,Q. and Lamb,C.J.
;   TITLE     Plant defense genes and plant defense regulatory elements
;   JOURNAL   Patent: US 5695939-A 25 09-DEC-1997;
; FEATURES             Location/Qualifiers
;      source          1. .10
;                      /organism="unknown"
; BASE COUNT        2 a      4 c      2 g      2 t
; ORIGIN
;
;   I84475  Length: 10  October 2, 2003 14:56  Type: N  Check: 3874  ..
i84475

  Query Match             50.0%;  Score 10;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 8.9;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3322 AGGGGTTCCA 3331
              ||||||||||
Db         10 AGGGGTTCCA 1


RESULT 7
ax626783/c
;  TOIG of: ax626783  check: 4483  from: 1  to: 11
;
; LOCUS       AX626783                  11 bp    DNA     linear   PAT 21-FEB-2003
; DEFINITION  Sequence 3824 from Patent WO02053774.
; ACCESSION   AX626783
; VERSION     AX626783.1  GI:28454821
; KEYWORDS    .
; SOURCE      Homo sapiens (human)
;   ORGANISM  Homo sapiens
;             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
;             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
; REFERENCE   1
;   AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
;   TITLE     Method for determining homeostasis of the skin
;   JOURNAL   Patent: WO 02053774-A 3824 11-JUL-2002;
;             Henkel Kommanditgesellschaft auf Aktien (DE)
; FEATURES             Location/Qualifiers
;      source          1. .11
;                      /organism="Homo sapiens"
;                      /mol_type="genomic DNA"
;                      /db_xref="taxon:9606"
; BASE COUNT        2 a      6 c      2 g      1 t
; ORIGIN
;
;  AX626783  Length: 11  October 2, 2003 14:56  Type: N  Check: 4483  ..
ax626783

  Query Match             50.0%;  Score 10;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 8.1;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3323 GGGGTTCCAG 3332
              ||||||||||
Db         11 GGGGTTCCAG 2


RESULT 8
ax470549/c
;  TOIG of: ax470549  check: 4600  from: 1  to: 11
;
; LOCUS       AX470549                  11 bp    DNA     linear   PAT 09-AUG-2002
; DEFINITION  Sequence 126 from Patent WO02053773.
; ACCESSION   AX470549
; VERSION     AX470549.1  GI:22205674
; KEYWORDS    .
; SOURCE      Homo sapiens (human)
;   ORGANISM  Homo sapiens
;             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
;             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
; REFERENCE   1
;   AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
;   TITLE     Method for determining skin stress or skin ageing in vitro
;   JOURNAL   Patent: WO 02053773-A 126 11-JUL-2002;
;             HENKEL KGAA (DE)
; FEATURES             Location/Qualifiers
;      source          1. .11
;                      /organism="Homo sapiens"
;                      /mol_type="genomic DNA"
;                      /db_xref="taxon:9606"
; BASE COUNT        2 a      7 c      0 g      2 t
; ORIGIN
;
;  AX470549  Length: 11  October 2, 2003 14:56  Type: N  Check: 4600  ..
ax470549

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 10;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3315 GGGATTCAGGG 3325
              |||||| ||||
Db         11 GGGATTGAGGG 1


RESULT 9
ax623428/c
;  TOIG of: ax623428  check: 4600  from: 1  to: 11
;
; LOCUS       AX623428                  11 bp    DNA     linear   PAT 21-FEB-2003
; DEFINITION  Sequence 469 from Patent WO02053774.
; ACCESSION   AX623428
; VERSION     AX623428.1  GI:28451369
; KEYWORDS    .
; SOURCE      Homo sapiens (human)
;   ORGANISM  Homo sapiens
;             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
;             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
; REFERENCE   1
;   AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
;   TITLE     Method for determining homeostasis of the skin
;   JOURNAL   Patent: WO 02053774-A 469 11-JUL-2002;
;             Henkel Kommanditgesellschaft auf Aktien (DE)
; FEATURES             Location/Qualifiers
;      source          1. .11
;                      /organism="Homo sapiens"
;                      /mol_type="genomic DNA"
;                      /db_xref="taxon:9606"
; BASE COUNT        2 a      7 c      0 g      2 t
; ORIGIN
;
;  AX623428  Length: 11  October 2, 2003 14:56  Type: N  Check: 4600  ..
ax623428

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 10;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3315 GGGATTCAGGG 3325
              |||||| ||||
Db         11 GGGATTGAGGG 1


RESULT 10
```

```
ax629578
;  TOIG of: ax629578  check: 4860  from: 1  to: 11
;
; LOCUS       AX629578                 11 bp    DNA     linear   PAT 21-FEB-2003
; DEFINITION  Sequence 6619 from Patent WO02053774.
; ACCESSION   AX629578
; VERSION     AX629578.1  GI:28457616
; KEYWORDS    .
; SOURCE      Homo sapiens (human)
;   ORGANISM  Homo sapiens
;             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
;             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
; REFERENCE   1
;   AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
;   TITLE     Method for determining homeostasis of the skin
;   JOURNAL   Patent: WO 02053774-A 6619 11-JUL-2002;
;             Henkel Kommanditgesellschaft auf Aktien (DE)
; FEATURES             Location/Qualifiers
;      source          1. .11
;                      /organism="Homo sapiens"
;                      /mol_type="genomic DNA"
;                      /db_xref="taxon:9606"
; BASE COUNT        1 a      3 c      3 g      4 t
; ORIGIN
;
;  AX629578  Length: 11  October 2, 2003 14:56  Type: N  Check: 4860  ..
ax629578

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 10;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3319 TTCAGGGGTTC 3329
              ||||||| |||
Db          1 TTCAGGGCTTC 11


RESULT 11
ax630849/c
;  TOIG of: ax630849  check: 4600  from: 1  to: 11
;
; LOCUS       AX630849                 11 bp    DNA     linear   PAT 21-FEB-2003
; DEFINITION  Sequence 7890 from Patent WO02053774.
; ACCESSION   AX630849
; VERSION     AX630849.1  GI:28458889
; KEYWORDS    .
; SOURCE      Homo sapiens (human)
;   ORGANISM  Homo sapiens
;             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
;             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
; REFERENCE   1
;   AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
;   TITLE     Method for determining homeostasis of the skin
;   JOURNAL   Patent: WO 02053774-A 7890 11-JUL-2002;
;             Henkel Kommanditgesellschaft auf Aktien (DE)
; FEATURES             Location/Qualifiers
;      source          1. .11
;                      /organism="Homo sapiens"
;                      /mol_type="genomic DNA"
;                      /db_xref="taxon:9606"
; BASE COUNT        2 a      7 c      0 g      2 t
; ORIGIN
;
;  AX630849  Length: 11  October 2, 2003 14:56  Type: N  Check: 4600  ..
ax630849

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 10;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3315 GGGATTCAGGG 3325
              |||||| ||||
Db         11 GGGATTGAGGG 1


RESULT 12
e39766
;  TOIG of: e39766  check: 4052  from: 1  to: 10
;
; LOCUS       E39766                   10 bp    DNA     linear   PAT 31-JAN-2002
; DEFINITION  Genes with human dendritic cell expression.
; ACCESSION   E39766
; VERSION     E39766.1  GI:18621857
; KEYWORDS    JP 2000279181-A/299.
; SOURCE      Homo sapiens (human)
;   ORGANISM  Homo sapiens
;             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
;             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
; REFERENCE   1  (bases 1 to 10)
;   AUTHORS   Hashimoto,S., Matsushima,K. and Suzuki,T.
;   TITLE     Genes with human dendritic cell expression
;   JOURNAL   Patent: JP 2000279181-A 299 10-OCT-2000;
;             SCIENCE & TECH AGENCY
; COMMENT     OS   Homo sapiens (human)
;             PN   JP 2000279181-A/299
;             PD   10-OCT-2000
;             PF   01-APR-1999 JP 1999095481
;             PR
;             PI   SHINICHI HASHIMOTO,KOJI MATSUSHIMA,TAKUJI SUZUKI PC
;             C12N15/09,C07K14/475,C07K16/18,C12N15/00
;             CC
;             FH   Key             Location/Qualifiers
;             FT   source          1. .10
;             FT                   /organism='Homo sapiens (human)'.
; FEATURES             Location/Qualifiers
;      source          1. .10
;                      /organism="Homo sapiens"
;                      /mol_type="genomic DNA"
;                      /db_xref="taxon:9606"
; BASE COUNT        1 a      2 c      4 g      3 t
; ORIGIN
;
;   E39766  Length: 10  October 2, 2003 14:56  Type: N  Check: 4052  ..
e39766

  Query Match             45.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 13;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3324 GGGTTCCAG 3332
              |||||||||
Db          1 GGGTTCCAG 9


RESULT 13
ax471317
;  TOIG of: ax471317  check: 4715  from: 1  to: 11
;
; LOCUS       AX471317                 11 bp    DNA     linear   PAT 09-AUG-2002
; DEFINITION  Sequence 894 from Patent WO02053773.
; ACCESSION   AX471317
; VERSION     AX471317.1  GI:22206442
; KEYWORDS    .
; SOURCE      Homo sapiens (human)
;   ORGANISM  Homo sapiens
;             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
;             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
; REFERENCE   1
;   AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
;   TITLE     Method for determining skin stress or skin ageing in vitro
;   JOURNAL   Patent: WO 02053773-A 894 11-JUL-2002;
;             HENKEL KGAA (DE)
; FEATURES             Location/Qualifiers
;      source          1. .11
;                      /organism="Homo sapiens"
;                      /mol_type="genomic DNA"
;
```

```
;                     /db_xref="taxon:9606"
; BASE COUNT        2 a      2 c      5 g      2 t
; ORIGIN
;
;  AX471317  Length: 11  October 2, 2003 14:56  Type: N  Check: 4715  ..
ax471317

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3324 GGGTTCCAG 3332
              |||||||||
Db          3 GGGTTCCAG 11


RESULT 14
ax624360
;  TOIG of: ax624360  check: 4819  from: 1  to: 11
;
; LOCUS       AX624360                 11 bp    DNA     linear   PAT 21-FEB-2003
; DEFINITION  Sequence 1401 from Patent WO02053774.
; ACCESSION   AX624360
; VERSION     AX624360.1  GI:28452301
; KEYWORDS    .
; SOURCE      Homo sapiens (human)
;   ORGANISM  Homo sapiens
;             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
;             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
; REFERENCE   1
;   AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
;   TITLE     Method for determining homeostasis of the skin
;   JOURNAL   Patent: WO 02053774-A 1401 11-JUL-2002;
;             Henkel Kommanditgesellschaft auf Aktien (DE)
; FEATURES             Location/Qualifiers
;      source          1. .11
;                      /organism="Homo sapiens"
;                      /mol_type="genomic DNA"
;                      /db_xref="taxon:9606"
; BASE COUNT        1 a      3 c      3 g      4 t
; ORIGIN
;
;  AX624360  Length: 11  October 2, 2003 14:56  Type: N  Check: 4819  ..
ax624360

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3325 GGTTCCAGC 3333
              |||||||||
Db          2 GGTTCCAGC 10


RESULT 15
ax625683
;  TOIG of: ax625683  check: 4678  from: 1  to: 11
;
; LOCUS       AX625683                 11 bp    DNA     linear   PAT 21-FEB-2003
; DEFINITION  Sequence 2724 from Patent WO02053774.
; ACCESSION   AX625683
; VERSION     AX625683.1  GI:28453624
; KEYWORDS    .
; SOURCE      Homo sapiens (human)
;   ORGANISM  Homo sapiens
;             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
;             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
; REFERENCE   1
;   AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
;   TITLE     Method for determining homeostasis of the skin
;   JOURNAL   Patent: WO 02053774-A 2724 11-JUL-2002;
;             Henkel Kommanditgesellschaft auf Aktien (DE)
; FEATURES             Location/Qualifiers
;      source          1. .11
;                      /organism="Homo sapiens"
;                      /mol_type="genomic DNA"
;                      /db_xref="taxon:9606"
; BASE COUNT        2 a      2 c      4 g      3 t
; ORIGIN
;
;  AX625683  Length: 11  October 2, 2003 14:56  Type: N  Check: 4678  ..
ax625683

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3318 ATTCAGGGG 3326
              |||||||||
Db          2 ATTCAGGGG 10


RESULT 16
ax625706/c
;  TOIG of: ax625706  check: 4510  from: 1  to: 11
;
; LOCUS       AX625706                 11 bp    DNA     linear   PAT 21-FEB-2003
; DEFINITION  Sequence 2747 from Patent WO02053774.
; ACCESSION   AX625706
; VERSION     AX625706.1  GI:28453647
; KEYWORDS    .
; SOURCE      Homo sapiens (human)
;   ORGANISM  Homo sapiens
;             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
;             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
; REFERENCE   1
;   AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
;   TITLE     Method for determining homeostasis of the skin
;   JOURNAL   Patent: WO 02053774-A 2747 11-JUL-2002;
;             Henkel Kommanditgesellschaft auf Aktien (DE)
; FEATURES             Location/Qualifiers
;      source          1. .11
;                      /organism="Homo sapiens"
;                      /mol_type="genomic DNA"
;                      /db_xref="taxon:9606"
; BASE COUNT        2 a      4 c      4 g      1 t
; ORIGIN
;
;  AX625706  Length: 11  October 2, 2003 14:56  Type: N  Check: 4510  ..
ax625706

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3323 GGGGTTCCA 3331
              |||||||||
Db         10 GGGGTTCCA 2


RESULT 17
ax626201
;  TOIG of: ax626201  check: 4715  from: 1  to: 11
;
; LOCUS       AX626201                 11 bp    DNA     linear   PAT 21-FEB-2003
; DEFINITION  Sequence 3242 from Patent WO02053774.
; ACCESSION   AX626201
; VERSION     AX626201.1  GI:28454239
; KEYWORDS    .
; SOURCE      Homo sapiens (human)
;   ORGANISM  Homo sapiens
;             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
;             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
; REFERENCE   1
;   AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
;   TITLE     Method for determining homeostasis of the skin
```

```
;   JOURNAL   Patent: WO 02053774-A 3242 11-JUL-2002;
;             Henkel Kommanditgesellschaft auf Aktien (DE)
; FEATURES             Location/Qualifiers
;      source          1. .11
;                      /organism="Homo sapiens"
;                      /mol_type="genomic DNA"
;                      /db_xref="taxon:9606"
; BASE COUNT        2 a      2 c      5 g      2 t
; ORIGIN
;
;  AX626201  Length: 11  October 2, 2003 14:56  Type: N  Check: 4715  ..
ax626201

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3324 GGGTTCCAG 3332
              |||||||||
Db          3 GGGTTCCAG 11


RESULT 18
ax631781
;  TOIG of: ax631781  check: 4819  from: 1  to: 11
;
; LOCUS       AX631781                 11 bp    DNA     linear   PAT 21-FEB-2003
; DEFINITION  Sequence 8823 from Patent WO02053774.
; ACCESSION   AX631781
; VERSION     AX631781.1  GI:28459888
; KEYWORDS    .
; SOURCE      Homo sapiens (human)
;   ORGANISM  Homo sapiens
;             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
;             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
; REFERENCE   1
;   AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
;   TITLE     Method for determining homeostasis of the skin
;   JOURNAL   Patent: WO 02053774-A 8823 11-JUL-2002;
;             Henkel Kommanditgesellschaft auf Aktien (DE)
; FEATURES             Location/Qualifiers
;      source          1. .11
;                      /organism="Homo sapiens"
;                      /mol_type="genomic DNA"
;                      /db_xref="taxon:9606"
; BASE COUNT        1 a      3 c      3 g      4 t
; ORIGIN
;
;  AX631781  Length: 11  October 2, 2003 14:56  Type: N  Check: 4819  ..
ax631781

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3325 GGTTCCAGC 3333
              |||||||||
Db          2 GGTTCCAGC 10


RESULT 19
ar303398
;  TOIG of: ar303398  check: 3880  from: 1  to: 10
;
; LOCUS       AR303398                 10 bp    DNA     linear   PAT 12-JUN-2003
; DEFINITION  Sequence 123 from patent US 6544736.
; ACCESSION   AR303398
; VERSION     AR303398.1  GI:31692174
; KEYWORDS    .
; SOURCE      Unknown.
;   ORGANISM  Unknown.
;             Unclassified.
; REFERENCE   1  (bases 1 to 10)
;   AUTHORS   Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and
;             Watahiki,M.
;   TITLE     Method for synthesizing cDNA from mRNA sample
;   JOURNAL   Patent: US 6544736-A 123 08-APR-2003;
; FEATURES             Location/Qualifiers
;      source          1. .10
;                      /organism="unknown"
; BASE COUNT        3 a      1 c      4 g      2 t
; ORIGIN
;
;  AR303398  Length: 10  October 2, 2003 14:56  Type: N  Check: 3880  ..
ar303398

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 17;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3317 GATTCAGGGG 3326
              ||||||| ||
Db          1 GATTCAGAGG 10


RESULT 20
ar303424/c
;  TOIG of: ar303424  check: 3968  from: 1  to: 10
;
; LOCUS       AR303424                 10 bp    DNA     linear   PAT 12-JUN-2003
; DEFINITION  Sequence 149 from patent US 6544736.
; ACCESSION   AR303424
; VERSION     AR303424.1  GI:31692200
; KEYWORDS    .
; SOURCE      Unknown.
;   ORGANISM  Unknown.
;             Unclassified.
; REFERENCE   1  (bases 1 to 10)
;   AUTHORS   Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and
;             Watahiki,M.
;   TITLE     Method for synthesizing cDNA from mRNA sample
;   JOURNAL   Patent: US 6544736-A 149 08-APR-2003;
; FEATURES             Location/Qualifiers
;      source          1. .10
;                      /organism="unknown"
; BASE COUNT        2 a      4 c      1 g      3 t
; ORIGIN
;
;  AR303424  Length: 10  October 2, 2003 14:56  Type: N  Check: 3968  ..
ar303424

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 17;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3317 GATTCAGGGG 3326
              ||||||| ||
Db         10 GATTCAGAGG 1


RESULT 21
ax112965/c
;  TOIG of: ax112965  check: 3925  from: 1  to: 10
;
; LOCUS       AX112965                 10 bp    DNA     linear   PAT 01-MAY-2001
; DEFINITION  Sequence 12 from Patent WO0127267.
; ACCESSION   AX112965
; VERSION     AX112965.1  GI:13939400
; KEYWORDS    .
; SOURCE      Mus sp.
;   ORGANISM  Mus sp.
;             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
;             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
; REFERENCE   1
;   AUTHORS   Adams,E., Waldmann,H., Cobbold,S. and Zelenika,D.
;   TITLE     Genes differentially expressed in tr1 cells and their use in the
```

```
;            manufacture of immunoregulatory compositions
;   JOURNAL   Patent: WO 0127267-A 12 19-APR-2001;
;             ISIS INNOVATION LIMITED (GB)
; FEATURES             Location/Qualifiers
;      source          1. .10
;                      /organism="Mus sp."
;                      /mol_type="genomic DNA"
;                      /db_xref="taxon:10095"
; BASE COUNT        1 a      5 c      2 g      2 t
; ORIGIN
;
;  AX112965  Length: 10  October 2, 2003 14:56  Type: N  Check: 3925  ..
ax112965

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 17;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3316 GGATTCAGGG 3325
              ||| ||||||
Db         10 GGACTCAGGG 1


RESULT 22
ax152520
;  TOIG of: ax152520  check: 3920  from: 1  to: 10
;
; LOCUS       AX152520                 10 bp    DNA     linear   PAT 22-JUN-2001
; DEFINITION  Sequence 435 from Patent WO0138577.
; ACCESSION   AX152520
; VERSION     AX152520.1  GI:14534171
; KEYWORDS    .
; SOURCE      Homo sapiens (human)
;   ORGANISM  Homo sapiens
;             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
;             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
; REFERENCE   1
;   AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
;   TITLE     Human transcriptomes
;   JOURNAL   Patent: WO 0138577-A 435 31-MAY-2001;
;             The Johns Hopkins University (US)
; FEATURES             Location/Qualifiers
;      source          1. .10
;                      /organism="Homo sapiens"
;                      /mol_type="genomic DNA"
;                      /db_xref="taxon:9606"
; BASE COUNT        2 a      3 c      3 g      2 t
; ORIGIN
;
;  AX152520  Length: 10  October 2, 2003 14:56  Type: N  Check: 3920  ..
ax152520

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 17;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3322 AGGGGTTCCA 3331
              |||| |||||
Db          1 AGGGCTTCCA 10


RESULT 23
ax153581
;  TOIG of: ax153581  check: 3920  from: 1  to: 10
;
; LOCUS       AX153581                 10 bp    DNA     linear   PAT 22-JUN-2001
; DEFINITION  Sequence 1496 from Patent WO0138577.
; ACCESSION   AX153581
; VERSION     AX153581.1  GI:14535232
; KEYWORDS    .
; SOURCE      Homo sapiens (human)
;   ORGANISM  Homo sapiens
;             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
;             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
; REFERENCE   1
;   AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
;   TITLE     Human transcriptomes
;   JOURNAL   Patent: WO 0138577-A 1496 31-MAY-2001;
;             The Johns Hopkins University (US)
; FEATURES             Location/Qualifiers
;      source          1. .10
;                      /organism="Homo sapiens"
;                      /mol_type="genomic DNA"
;                      /db_xref="taxon:9606"
; BASE COUNT        2 a      3 c      3 g      2 t
; ORIGIN
;
;  AX153581  Length: 10  October 2, 2003 14:56  Type: N  Check: 3920  ..
ax153581

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 17;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3322 AGGGGTTCCA 3331
              |||| |||||
Db          1 AGGGCTTCCA 10


RESULT 24
ax153631
;  TOIG of: ax153631  check: 3920  from: 1  to: 10
;
; LOCUS       AX153631                 10 bp    DNA     linear   PAT 22-JUN-2001
; DEFINITION  Sequence 1546 from Patent WO0138577.
; ACCESSION   AX153631
; VERSION     AX153631.1  GI:14535282
; KEYWORDS    .
; SOURCE      Homo sapiens (human)
;   ORGANISM  Homo sapiens
;             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
;             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
; REFERENCE   1
;   AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
;   TITLE     Human transcriptomes
;   JOURNAL   Patent: WO 0138577-A 1546 31-MAY-2001;
;             The Johns Hopkins University (US)
; FEATURES             Location/Qualifiers
;      source          1. .10
;                      /organism="Homo sapiens"
;                      /mol_type="genomic DNA"
;                      /db_xref="taxon:9606"
; BASE COUNT        2 a      3 c      3 g      2 t
; ORIGIN
;
;  AX153631  Length: 10  October 2, 2003 14:56  Type: N  Check: 3920  ..
ax153631

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 17;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3322 AGGGGTTCCA 3331
              |||| |||||
Db          1 AGGGCTTCCA 10


RESULT 25
ax301326
;  TOIG of: ax301326  check: 3920  from: 1  to: 10
;
; LOCUS       AX301326                 10 bp    DNA     linear   PAT 30-NOV-2001
; DEFINITION  Sequence 40 from Patent WO0185941.
; ACCESSION   AX301326
; VERSION     AX301326.1  GI:17382409
; KEYWORDS    .
```

```
; SOURCE      Homo sapiens (human)
;   ORGANISM  Homo sapiens
;             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
;             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
; REFERENCE   1
;   AUTHORS   Versteeg,R. and Caron,H.N.
;   TITLE     Myc targets
;   JOURNAL   Patent: WO 0185941-A 40 15-NOV-2001;
;             Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
; FEATURES             Location/Qualifiers
;      source          1. .10
;                      /organism="Homo sapiens"
;                      /mol_type="genomic DNA"
;                      /db_xref="taxon:9606"
; BASE COUNT        2 a      3 c      3 g      2 t
; ORIGIN
;
;  AX301326  Length: 10  October 2, 2003 14:56  Type: N  Check: 3920  ..
ax301326

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 17;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3322 AGGGGTTCCA 3331
              |||| |||||
Db          1 AGGGCTTCCA 10


RESULT 26
ax667821
;  TOIG of: ax667821  check: 3978  from: 1  to: 10
;
; LOCUS       AX667821                 10 bp    DNA     linear   PAT 26-MAR-2003
; DEFINITION  Sequence 1270 from Patent WO0242459.
; ACCESSION   AX667821
; VERSION     AX667821.1  GI:29291358
; KEYWORDS    .
; SOURCE      synthetic construct
;   ORGANISM  synthetic construct
;             artificial sequences.
; REFERENCE   1
;   AUTHORS   Liu,Q.
;   TITLE     Position dependent recognition of gnn nucleotide triplets by zinc
;             fingers
;   JOURNAL   Patent: WO 0242459-A 1270 30-MAY-2002;
;             Sangamo Biosciences Inc. (US)
; FEATURES             Location/Qualifiers
;      source          1. .10
;                      /organism="synthetic construct"
;                      /mol_type="genomic DNA"
;                      /db_xref="taxon:32630"
;                      /note="example target DNA"
; BASE COUNT        3 a      1 c      3 g      3 t
; ORIGIN
;
;  AX667821  Length: 10  October 2, 2003 14:56  Type: N  Check: 3978  ..
ax667821

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 17;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3314 AGGGATTCAG 3323
              | ||||||||
Db          1 ATGGATTCAG 10


RESULT 27
ax667826
;  TOIG of: ax667826  check: 3978  from: 1  to: 10
;
; LOCUS       AX667826                 10 bp    DNA     linear   PAT 26-MAR-2003
; DEFINITION  Sequence 1275 from Patent WO0242459.
; ACCESSION   AX667826
; VERSION     AX667826.1  GI:29291363
; KEYWORDS    .
; SOURCE      synthetic construct
;   ORGANISM  synthetic construct
;             artificial sequences.
; REFERENCE   1
;   AUTHORS   Liu,Q.
;   TITLE     Position dependent recognition of gnn nucleotide triplets by zinc
;             fingers
;   JOURNAL   Patent: WO 0242459-A 1275 30-MAY-2002;
;             Sangamo Biosciences Inc. (US)
; FEATURES             Location/Qualifiers
;      source          1. .10
;                      /organism="synthetic construct"
;                      /mol_type="genomic DNA"
;                      /db_xref="taxon:32630"
;                      /note="example target DNA"
; BASE COUNT        3 a      1 c      3 g      3 t
; ORIGIN
;
;  AX667826  Length: 10  October 2, 2003 14:56  Type: N  Check: 3978  ..
ax667826

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 17;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3314 AGGGATTCAG 3323
              | ||||||||
Db          1 ATGGATTCAG 10


RESULT 28
ax667888
;  TOIG of: ax667888  check: 3978  from: 1  to: 10
;
; LOCUS       AX667888                 10 bp    DNA     linear   PAT 26-MAR-2003
; DEFINITION  Sequence 1337 from Patent WO0242459.
; ACCESSION   AX667888
; VERSION     AX667888.1  GI:29291425
; KEYWORDS    .
; SOURCE      synthetic construct
;   ORGANISM  synthetic construct
;             artificial sequences.
; REFERENCE   1
;   AUTHORS   Liu,Q.
;   TITLE     Position dependent recognition of gnn nucleotide triplets by zinc
;             fingers
;   JOURNAL   Patent: WO 0242459-A 1337 30-MAY-2002;
;             Sangamo Biosciences Inc. (US)
; FEATURES             Location/Qualifiers
;      source          1. .10
;                      /organism="synthetic construct"
;                      /mol_type="genomic DNA"
;                      /db_xref="taxon:32630"
;                      /note="example target DNA"
; BASE COUNT        3 a      1 c      3 g      3 t
; ORIGIN
;
;  AX667888  Length: 10  October 2, 2003 14:56  Type: N  Check: 3978  ..
ax667888

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 17;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3314 AGGGATTCAG 3323
              | ||||||||
Db          1 ATGGATTCAG 10
```

```
RESULT 29
bd007762
;  TOIG of: bd007762  check: 3920  from: 1  to: 10
;
; LOCUS       BD007762                 10 bp    DNA     linear   PAT 31-JAN-2002
; DEFINITION  LPS activated human monocyte expressing genes.
; ACCESSION   BD007762
; VERSION     BD007762.1  GI:18636135
; KEYWORDS    JP 2001069993-A/38.
; SOURCE      Homo sapiens (human)
;   ORGANISM  Homo sapiens
;             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
;             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
; REFERENCE   1  (bases 1 to 10)
;   AUTHORS   Matsushima,K., Hashimoto,S. and Suzuki,T.
;   TITLE     LPS activated human monocyte expressing genes
;   JOURNAL   Patent: JP 2001069993-A 38 21-MAR-2001;
;             JAPAN SCIENCE AND TECHNOLOGY CORP
; COMMENT     OS   Homo sapiens (human)
;             PN   JP 2001069993-A/38
;             PD   21-MAR-2001
;             PF   28-APR-2000 JP 2000131079
;             PR
;             PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
;             C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC
;             A61P29/00,
;             PC   A61P31/00,C12P21/08,C12N15/00
;             CC
;             FH   Key             Location/Qualifiers
;             FT   source          1. .10
;             FT                   /organism='Homo sapiens (human)'.
; FEATURES             Location/Qualifiers
;      source          1. .10
;                      /organism="Homo sapiens"
;                      /mol_type="genomic DNA"
;                      /db_xref="taxon:9606"
; BASE COUNT        2 a      3 c      3 g      2 t
; ORIGIN
;
;  BD007762  Length: 10  October 2, 2003 14:56  Type: N  Check: 3920  ..
bd007762

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 17;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3322 AGGGGTTCCA 3331
              |||| |||||
Db          1 AGGGCTTCCA 10


RESULT 30
bd007794/c
;  TOIG of: bd007794  check: 3919  from: 1  to: 10
;
; LOCUS       BD007794                 10 bp    DNA     linear   PAT 31-JAN-2002
; DEFINITION  LPS activated human monocyte expressing genes.
; ACCESSION   BD007794
; VERSION     BD007794.1  GI:18636167
; KEYWORDS    JP 2001069993-A/70.
; SOURCE      Homo sapiens (human)
;   ORGANISM  Homo sapiens
;             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
;             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
; REFERENCE   1  (bases 1 to 10)
;   AUTHORS   Matsushima,K., Hashimoto,S. and Suzuki,T.
;   TITLE     LPS activated human monocyte expressing genes
;   JOURNAL   Patent: JP 2001069993-A 70 21-MAR-2001;
;             JAPAN SCIENCE AND TECHNOLOGY CORP
; COMMENT     OS   Homo sapiens (human)
;             PN   JP 2001069993-A/70
;             PD   21-MAR-2001
;             PF   28-APR-2000 JP 2000131079
;             PR
;             PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
;             C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC
;             A61P29/00,
;             PC   A61P31/00,C12P21/08,C12N15/00
;             CC
;             FH   Key             Location/Qualifiers
;             FT   source          1. .10
;             FT                   /organism='Homo sapiens (human)'.
; FEATURES             Location/Qualifiers
;      source          1. .10
;                      /organism="Homo sapiens"
;                      /mol_type="genomic DNA"
;                      /db_xref="taxon:9606"
; BASE COUNT        1 a      5 c      2 g      2 t
; ORIGIN
;
;  BD007794  Length: 10  October 2, 2003 14:56  Type: N  Check: 3919  ..
bd007794

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 17;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3316 GGATTCAGGG 3325
              |||| |||||
Db         10 GGATCCAGGG 1


RESULT 31
bd083142
;  TOIG of: bd083142  check: 3920  from: 1  to: 10
;
; LOCUS       BD083142                 10 bp    DNA     linear   PAT 27-AUG-2002
; DEFINITION  Human matured/activated dendritic cell expression genes.
; ACCESSION   BD083142
; VERSION     BD083142.1  GI:22628752
; KEYWORDS    JP 2001327293-A/63.
; SOURCE      Homo sapiens (human)
;   ORGANISM  Homo sapiens
;             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
;             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
; REFERENCE   1  (bases 1 to 10)
;   AUTHORS   Matsushima,K., Hashimoto,S., Suzuki,T. and Nagai,S.
;   TITLE     Human matured/activated dendritic cell expression genes
;   JOURNAL   Patent: JP 2001327293-A 63 27-NOV-2001;
;             JAPAN SCIENCE AND TECHNOLOGY CORP
; COMMENT     OS   Homo sapiens (human)
;             PN   JP 2001327293-A/63
;             PD   27-NOV-2001
;             PF   22-MAY-2000 JP 2000150562
;             PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI,SHIGENORI  PI
;               NAGAI
;             PC   C12N15/09,C07K14/47,C07K16/18//C12P21/02,C12P21/08,C12N15/00
;             CC
;             FH   Key             Location/Qualifiers.
; FEATURES             Location/Qualifiers
;      source          1. .10
;                      /organism="Homo sapiens"
;                      /mol_type="genomic DNA"
;                      /db_xref="taxon:9606"
; BASE COUNT        2 a      3 c      3 g      2 t
; ORIGIN
;
;  BD083142  Length: 10  October 2, 2003 14:56  Type: N  Check: 3920  ..
bd083142

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 17;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3322 AGGGGTTCCA 3331
              |||| |||||
```

```
Db          1 AGGGCTTCCA 10


RESULT 32
bd083204/c
;  TOIG of: bd083204  check: 3846  from: 1  to: 10
;
; LOCUS       BD083204                 10 bp    DNA     linear   PAT 27-AUG-2002
; DEFINITION  Human matured/activated dendritic cell expression genes.
; ACCESSION   BD083204
; VERSION     BD083204.1  GI:22628814
; KEYWORDS    JP 2001327293-A/125.
; SOURCE      Homo sapiens (human)
;   ORGANISM  Homo sapiens
;             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
;             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
; REFERENCE   1  (bases 1 to 10)
;   AUTHORS   Matsushima,K., Hashimoto,S., Suzuki,T. and Nagai,S.
;   TITLE     Human matured/activated dendritic cell expression genes
;   JOURNAL   Patent: JP 2001327293-A 125 27-NOV-2001;
;             JAPAN SCIENCE AND TECHNOLOGY CORP
; COMMENT     OS   Homo sapiens (human)
;             PN   JP 2001327293-A/125
;             PD   27-NOV-2001
;             PF   22-MAY-2000 JP 2000150562
;             PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI,SHIGENORI  PI
;               NAGAI
;             PC   C12N15/09,C07K14/47,C07K16/18//C12P21/02,C12P21/08,C12N15/00
;             CC
;             FH   Key            Location/Qualifiers.
; FEATURES            Location/Qualifiers
;      source         1. .10
;                     /organism="Homo sapiens"
;                     /mol_type="genomic DNA"
;                     /db_xref="taxon:9606"
; BASE COUNT        3 a      4 c      2 g      1 t
; ORIGIN
;
;  BD083204  Length: 10  October 2, 2003 14:56  Type: N  Check: 3846  ..
bd083204

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 17;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3319 TTCAGGGGTT 3328
              | ||||||||
Db         10 TCCAGGGGTT 1


RESULT 33
bd083268/c
;  TOIG of: bd083268  check: 3919  from: 1  to: 10
;
; LOCUS       BD083268                 10 bp    DNA     linear   PAT 27-AUG-2002
; DEFINITION  Human matured/activated dendritic cell expression genes.
; ACCESSION   BD083268
; VERSION     BD083268.1  GI:22628878
; KEYWORDS    JP 2001327293-A/189.
; SOURCE      Homo sapiens (human)
;   ORGANISM  Homo sapiens
;             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
;             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
; REFERENCE   1  (bases 1 to 10)
;   AUTHORS   Matsushima,K., Hashimoto,S., Suzuki,T. and Nagai,S.
;   TITLE     Human matured/activated dendritic cell expression genes
;   JOURNAL   Patent: JP 2001327293-A 189 27-NOV-2001;
;             JAPAN SCIENCE AND TECHNOLOGY CORP
; COMMENT     OS   Homo sapiens (human)
;             PN   JP 2001327293-A/189
;             PD   27-NOV-2001
;             PF   22-MAY-2000 JP 2000150562
;             PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI,SHIGENORI  PI
;               NAGAI
;             PC   C12N15/09,C07K14/47,C07K16/18//C12P21/02,C12P21/08,C12N15/00
;             CC
;             FH   Key            Location/Qualifiers.
; FEATURES            Location/Qualifiers
;      source         1. .10
;                     /organism="Homo sapiens"
;                     /mol_type="genomic DNA"
;                     /db_xref="taxon:9606"
; BASE COUNT        1 a      5 c      2 g      2 t
; ORIGIN
;
;  BD083268  Length: 10  October 2, 2003 14:56  Type: N  Check: 3919  ..
bd083268

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 17;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3316 GGATTCAGGG 3325
              |||| |||||
Db         10 GGATCCAGGG 1


RESULT 34
e39536
;  TOIG of: e39536  check: 3920  from: 1  to: 10
;
; LOCUS       E39536                   10 bp    DNA     linear   PAT 31-JAN-2002
; DEFINITION  Genes with human dendritic cell expression.
; ACCESSION   E39536
; VERSION     E39536.1  GI:18621627
; KEYWORDS    JP 2000279181-A/69.
; SOURCE      Homo sapiens (human)
;   ORGANISM  Homo sapiens
;             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
;             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
; REFERENCE   1  (bases 1 to 10)
;   AUTHORS   Hashimoto,S., Matsushima,K. and Suzuki,T.
;   TITLE     Genes with human dendritic cell expression
;   JOURNAL   Patent: JP 2000279181-A 69 10-OCT-2000;
;             SCIENCE & TECH AGENCY
; COMMENT     OS   Homo sapiens (human)
;             PN   JP 2000279181-A/69
;             PD   10-OCT-2000
;             PF   01-APR-1999 JP 1999095481
;             PR
;             PI   SHINICHI HASHIMOTO,KOJI MATSUSHIMA,TAKUJI SUZUKI PC
;             C12N15/09,C07K14/475,C07K16/18,C12N15/00
;             CC
;             FH   Key            Location/Qualifiers
;             FT   source         1. .10
;             FT                  /organism='Homo sapiens (human)'.
; FEATURES            Location/Qualifiers
;      source         1. .10
;                     /organism="Homo sapiens"
;                     /mol_type="genomic DNA"
;                     /db_xref="taxon:9606"
; BASE COUNT        2 a      3 c      3 g      2 t
; ORIGIN
;
;  E39536  Length: 10  October 2, 2003 14:56  Type: N  Check: 3920  ..
e39536

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 17;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3322 AGGGGTTCCA 3331
              |||| |||||
Db          1 AGGGCTTCCA 10
```

```
RESULT 35
e54753
;  TOIG of: e54753  check: 3920  from: 1  to: 10
;
; LOCUS       E54753                    10 bp    DNA     linear   PAT 27-AUG-2002
; DEFINITION  Human normal liver cell expression genes.
; ACCESSION   E54753
; VERSION     E54753.1  GI:22556236
; KEYWORDS    JP 2001211883-A/105.
; SOURCE      Homo sapiens (human)
;   ORGANISM  Homo sapiens
;             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
;             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
; REFERENCE   1  (bases 1 to 10)
;   AUTHORS   Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
;   TITLE     Human normal liver cell expression genes
;   JOURNAL   Patent: JP 2001211883-A 105 07-AUG-2001;
;             SCIENCE & TECH AGENCY
; COMMENT     OS   Homo sapiens (human)
;             PN   JP 2001211883-A/105
;             PD   07-AUG-2001
;             PF   31-JAN-2000 JP 2000023170
;             PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO  PI
;             YAMASHITA
;             PC   C12N15/09,C07K16/18,C12P21/02,C12N15/00
;             CC
;             FH   Key             Location/Qualifiers.
; FEATURES             Location/Qualifiers
;      source          1. .10
;                      /organism="Homo sapiens"
;                      /mol_type="genomic DNA"
;                      /db_xref="taxon:9606"
; BASE COUNT        2 a      3 c      3 g      2 t
; ORIGIN
;
;   E54753  Length: 10  October 2, 2003 14:56  Type: N  Check: 3920  ..
e54753

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 17;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3322 AGGGGTTCCA 3331
              |||| |||||
Db          1 AGGGCTTCCA 10


RESULT 36
ar017955
;  TOIG of: ar017955  check: 4214  from: 1  to: 10
;
; LOCUS       AR017955                  10 bp    DNA     linear   PAT 05-DEC-1998
; DEFINITION  Sequence 20 from patent US 5780273.
; ACCESSION   AR017955
; VERSION     AR017955.1  GI:3973558
; KEYWORDS    .
; SOURCE      Unknown.
;   ORGANISM  Unknown.
;             Unclassified.
; REFERENCE   1  (bases 1 to 10)
;   AUTHORS   Burg,J.Lawrence.
;   TITLE     Insertion elements and amplifiable nucleic acids
;   JOURNAL   Patent: US 5780273-A 20 14-JUL-1998;
; FEATURES             Location/Qualifiers
;      source          1. .10
;                      /organism="unknown"
; BASE COUNT        1 a      1 c      5 g      3 t
; ORIGIN
;
;  AR017955  Length: 10  October 2, 2003 14:56  Type: N  Check: 4214  ..
ar017955

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 19;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3321 CAGGGGTT 3328
              ||||||||
Db          1 CAGGGGTT 8


RESULT 37
ar303474
;  TOIG of: ar303474  check: 3970  from: 1  to: 10
;
; LOCUS       AR303474                  10 bp    DNA     linear   PAT 12-JUN-2003
; DEFINITION  Sequence 199 from patent US 6544736
; ACCESSION   AR303474
; VERSION     AR303474.1  GI:31692250
; KEYWORDS    .
; SOURCE      Unknown.
;   ORGANISM  Unknown.
;             Unclassified.
; REFERENCE   1  (bases 1 to 10)
;   AUTHORS   Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and
;             Watahiki,M.
;   TITLE     Method for synthesizing cDNA from mRNA sample
;   JOURNAL   Patent: US 6544736-A 199 08-APR-2003;
; FEATURES             Location/Qualifiers
;      source          1. .10
;                      /organism="unknown"
; BASE COUNT        2 a      2 c      3 g      3 t
; ORIGIN
;
;  AR303474  Length: 10  October 2, 2003 14:56  Type: N  Check: 3970  ..
ar303474

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 19;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3317 GATTCAGG 3324
              ||||||||
Db          3 GATTCAGG 10


RESULT 38
ar303528/c
;  TOIG of: ar303528  check: 3871  from: 1  to: 10
;
; LOCUS       AR303528                  10 bp    DNA     linear   PAT 12-JUN-2003
; DEFINITION  Sequence 253 from patent US 6544736.
; ACCESSION   AR303528
; VERSION     AR303528.1  GI:31692304
; KEYWORDS    .
; SOURCE      Unknown.
;   ORGANISM  Unknown.
;             Unclassified.
; REFERENCE   1  (bases 1 to 10)
;   AUTHORS   Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and
;             Watahiki,M.
;   TITLE     Method for synthesizing cDNA from mRNA sample
;   JOURNAL   Patent: US 6544736-A 253 08-APR-2003;
; FEATURES             Location/Qualifiers
;      source          1. .10
;                      /organism="unknown"
; BASE COUNT        3 a      3 c      2 g      2 t
; ORIGIN
;
;  AR303528  Length: 10  October 2, 2003 14:56  Type: N  Check: 3871  ..
ar303528

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 19;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy       3317 GATTCAGG 3324
             ||||||||
Db          8 GATTCAGG 1


RESULT 39
ax152673
;  TOIG of: ax152673  check: 3877  from: 1  to: 10
;
; LOCUS       AX152673                 10 bp    DNA     linear   PAT 22-JUN-2001
; DEFINITION  Sequence 588 from Patent WO0138577.
; ACCESSION   AX152673
; VERSION     AX152673.1  GI:14534324
; KEYWORDS    .
; SOURCE      Homo sapiens (human)
;   ORGANISM  Homo sapiens
;             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
;             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
; REFERENCE   1
;   AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
;   TITLE     Human transcriptomes
;   JOURNAL   Patent: WO 0138577-A 588 31-MAY-2001;
;             The Johns Hopkins University (US)
; FEATURES             Location/Qualifiers
;      source          1. .10
;                      /organism="Homo sapiens"
;                      /mol_type="genomic DNA"
;                      /db_xref="taxon:9606"
; BASE COUNT        2 a      1 c      4 g      3 t
; ORIGIN
;
;  AX152673  Length: 10  October 2, 2003 14:56  Type: N  Check: 3877  ..
ax152673

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 19;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3319 TTCAGGGG 3326
             ||||||||
Db          2 TTCAGGGG 9


RESULT 40
ax301451
;  TOIG of: ax301451  check: 3877  from: 1  to: 10
;
; LOCUS       AX301451                 10 bp    DNA     linear   PAT 30-NOV-2001
; DEFINITION  Sequence 165 from Patent WO0185941.
; ACCESSION   AX301451
; VERSION     AX301451.1  GI:17382534
; KEYWORDS    .
; SOURCE      Homo sapiens (human)
;   ORGANISM  Homo sapiens
;             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
;             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
; REFERENCE   1
;   AUTHORS   Versteeg,R. and Caron,H.N.
;   TITLE     Myc targets
;   JOURNAL   Patent: WO 0185941-A 165 15-NOV-2001;
;             Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
; FEATURES             Location/Qualifiers
;      source          1. .10
;                      /organism="Homo sapiens"
;                      /mol_type="genomic DNA"
;                      /db_xref="taxon:9606"
; BASE COUNT        2 a      1 c      4 g      3 t
; ORIGIN
;
;  AX301451  Length: 10  October 2, 2003 14:56  Type: N  Check: 3877  ..
ax301451

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 19;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3319 TTCAGGGG 3326
             ||||||||
Db          2 TTCAGGGG 9


RESULT 41
ax301542
;  TOIG of: ax301542  check: 3877  from: 1  to: 10
;
; LOCUS       AX301542                 10 bp    DNA     linear   PAT 30-NOV-2001
; DEFINITION  Sequence 256 from Patent WO0185941.
; ACCESSION   AX301542
; VERSION     AX301542.1  GI:17382625
; KEYWORDS    .
; SOURCE      Homo sapiens (human)
;   ORGANISM  Homo sapiens
;             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
;             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
; REFERENCE   1
;   AUTHORS   Versteeg,R. and Caron,H.N.
;   TITLE     Myc targets
;   JOURNAL   Patent: WO 0185941-A 256 15-NOV-2001;
;             Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
; FEATURES             Location/Qualifiers
;      source          1. .10
;                      /organism="Homo sapiens"
;                      /mol_type="genomic DNA"
;                      /db_xref="taxon:9606"
; BASE COUNT        2 a      1 c      4 g      3 t
; ORIGIN
;
;  AX301542  Length: 10  October 2, 2003 14:56  Type: N  Check: 3877  ..
ax301542

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 19;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3319 TTCAGGGG 3326
             ||||||||
Db          2 TTCAGGGG 9


RESULT 42
ax719148
;  TOIG of: ax719148  check: 3981  from: 1  to: 10
;
; LOCUS       AX719148                 10 bp    DNA     linear   PAT 15-APR-2003
; DEFINITION  Sequence 20 from Patent EP1295950.
; ACCESSION   AX719148
; VERSION     AX719148.1  GI:29891635
; KEYWORDS    .
; SOURCE      Cucumis sativus (cucumber)
;   ORGANISM  Cucumis sativus
;             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
;             Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
;             rosids; eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
; REFERENCE   1
;   AUTHORS   Langeveld,S.A., van der Kop,D.A. and de Boer,A.D.
;   TITLE     Expression profiling
;   JOURNAL   Patent: EP 1295950-A 20 26-MAR-2003;
;             GT Diagnostics B.V. (NL)
; FEATURES             Location/Qualifiers
;      source          1. .10
;                      /organism="Cucumis sativus"
;                      /mol_type="genomic DNA"
;                      /db_xref="taxon:3659"
;      misc_feature    1. .10
;                      /note="Part of template RPL10 = sequence to analyze"
; BASE COUNT        2 a      1 c      4 g      3 t
```

; ORIGIN
;
; AX719148 Length: 10 October 2, 2003 14:56 Type: N Check: 3981 ..
ax719148

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       3315 GGGATTCA 3322
              ||||||||
Db          3 GGGATTCA 10
```

Search completed: October 2, 2003, 15:32:19
Job time : 1 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: October 2, 2003, 15:35:57 ; Search time 0.001 Seconds
(without alignments)
36.640 Million cell updates/sec

Title: us-09-676-436-3
Perfect score: 20
Sequence: 1 agggattcaggggttccagc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 89 seqs, 916 residues

Total number of hits satisfying chosen parameters: 178

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 89 summaries

Database : rng.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	20	100.0	20	1	aad37150	TOIG of: aad3715
	2	12.4	62.0	14	1	aaq83338	TOIG of: aaq8333
c	3	11	55.0	11	1	abq87435	TOIG of: abq8743
c	4	11	55.0	11	1	abv67711	TOIG of: abv6771
c	5	10	50.0	10	1	aaz83859	TOIG of: aaz8385
c	6	10	50.0	11	1	abv66038	TOIG of: abv6603
c	7	9.4	47.0	11	1	aal42209	TOIG of: aal4220
c	8	9.4	47.0	11	1	abq86371	TOIG of: abq8637
c	9	9.4	47.0	11	1	abv62683	TOIG of: abv6268
	10	9.4	47.0	11	1	abv68833	TOIG of: abv6883
c	11	9.4	47.0	11	1	abv70104	TOIG of: abv7010
	12	9	45.0	10	1	aac74212	TOIG of: aac7421
	13	9	45.0	10	1	aaf42053	TOIG of: aaf4205
c	14	9	45.0	10	1	aal48142	TOIG of: aal4814
c	15	9	45.0	10	1	aaz83465	TOIG of: aaz8346
	16	9	45.0	10	1	aaz84256	TOIG of: aaz8425
c	17	9	45.0	10	1	abk64082	TOIG of: abk6408
c	18	9	45.0	11	1	aaf30844	TOIG of: aaf3084
	19	9	45.0	11	1	abq87139	TOIG of: abq8713
	20	9	45.0	11	1	abv63615	TOIG of: abv6361
	21	9	45.0	11	1	abv64938	TOIG of: abv6493
c	22	9	45.0	11	1	abv64961	TOIG of: abv6496
	23	9	45.0	11	1	abv65456	TOIG of: abv6545
	24	9	45.0	11	1	abv71036	TOIG of: abv7103
	25	8.4	42.0	10	1	aaa56134	TOIG of: aaa5613
	26	8.4	42.0	10	1	aaa56289	TOIG of: aaa5628
	27	8.4	42.0	10	1	aaa56391	TOIG of: aaa5639
	28	8.4	42.0	10	1	aac73982	TOIG of: aac7398
	29	8.4	42.0	10	1	aaf36987	TOIG of: aaf3698
	30	8.4	42.0	10	1	aaf39730	TOIG of: aaf3973
c	31	8.4	42.0	10	1	aaf41037	TOIG of: aaf4103
c	32	8.4	42.0	10	1	aah19941	TOIG of: aah1994
	33	8.4	42.0	10	1	aah32665	TOIG of: aah3266
c	34	8.4	42.0	10	1	aah32697	TOIG of: aah3269
	35	8.4	42.0	10	1	aah63595	TOIG of: aah6359
	36	8.4	42.0	10	1	aah64656	TOIG of: aah6465
	37	8.4	42.0	10	1	aah64706	TOIG of: aah6470
c	38	8.4	42.0	10	1	aai67389	TOIG of: aai6738
c	39	8.4	42.0	10	1	aas19576	TOIG of: aas1957
	40	8.4	42.0	10	1	aas57315	TOIG of: aas5731
c	41	8.4	42.0	10	1	aav35904	TOIG of: aav3590
c	42	8.4	42.0	10	1	aaz83394	TOIG of: aaz8339
c	43	8.4	42.0	10	1	aaz83550	TOIG of: aaz8355
	44	8.4	42.0	10	1	aaz84309	TOIG of: aaz8430
c	45	8.4	42.0	10	1	aaz84773	TOIG of: aaz8477
c	46	8.4	42.0	10	1	aaz85387	TOIG of: aaz8538
c	47	8.4	42.0	10	1	aaz85591	TOIG of: aaz8559
c	48	8.4	42.0	10	1	aaz85716	TOIG of: aaz8571
	49	8.4	42.0	10	1	aba06128	TOIG of: aba0612
	50	8.4	42.0	10	1	abk23413	TOIG of: abk2341
	51	8.4	42.0	10	1	abk85685	TOIG of: abk8568
	52	8.4	42.0	10	1	abl42689	TOIG of: abl4268
c	53	8.4	42.0	10	1	abl42751	TOIG of: abl4275
c	54	8.4	42.0	10	1	abl42815	TOIG of: abl4281
	55	8.4	42.0	10	1	abq71536	TOIG of: abq7153
	56	8.4	42.0	10	1	abq71541	TOIG of: abq7154
	57	8.4	42.0	10	1	abq71603	TOIG of: abq7160
c	58	8	40.0	8	1	aaa80926	TOIG of: aaa8092
	59	8	40.0	10	1	aad45882	TOIG of: aad4588
	60	8	40.0	10	1	aaf35691	TOIG of: aaf3569
c	61	8	40.0	10	1	aaf36466	TOIG of: aaf3646
c	62	8	40.0	10	1	aaf40055	TOIG of: aaf4005
	63	8	40.0	10	1	aaf42054	TOIG of: aaf4205
	64	8	40.0	10	1	aaf42057	TOIG of: aaf4205
	65	8	40.0	10	1	aaf42631	TOIG of: aaf4263
c	66	8	40.0	10	1	aaf42841	TOIG of: aaf4284
	67	8	40.0	10	1	aah63748	TOIG of: aah6374
	68	8	40.0	10	1	aaq63560	TOIG of: aaq6356
c	69	8	40.0	10	1	aaz78096	TOIG of: aaz7809
	70	8	40.0	10	1	aaz78337	TOIG of: aaz7833
	71	8	40.0	10	1	aaz78909	TOIG of: aaz7890
c	72	8	40.0	10	1	aaz81683	TOIG of: aaz8168
c	73	8	40.0	10	1	aaz82371	TOIG of: aaz8237
c	74	8	40.0	10	1	aaz83968	TOIG of: aaz8396
	75	8	40.0	10	1	aaz84127	TOIG of: aaz8412
	76	8	40.0	10	1	aaz84157	TOIG of: aaz8415
c	77	8	40.0	10	1	aaz84158	TOIG of: aaz8415
c	78	8	40.0	10	1	aaz84257	TOIG of: aaz8425
c	79	8	40.0	10	1	aaz84401	TOIG of: aaz8440
	80	8	40.0	10	1	aaz84685	TOIG of: aaz8468
	81	8	40.0	10	1	aaz85131	TOIG of: aaz8513
c	82	8	40.0	10	1	aaz85236	TOIG of: aaz8523
	83	8	40.0	10	1	abk14251	TOIG of: abk1425
	84	8	40.0	10	1	abk23538	TOIG of: abk2353
	85	8	40.0	10	1	abk23629	TOIG of: abk2362
c	86	8	40.0	10	1	abk92637	TOIG of: abk9263
c	87	8	40.0	10	1	abk96539	TOIG of: abk9653
c	88	8	40.0	10	1	abt14312	TOIG of: abt1431
c	89	7.4	37.0	9	1	aav04711	TOIG of: aav0471

ALIGNMENTS

RESULT 1
aad37150/c
; TOIG of: aad37150 check: 4945 from: 1 to: 20
;
; ID AAD37150 standard; DNA; 20 BP.
; XX
; AC AAD37150;
; XX
; DT 21-AUG-2002 (first entry)
; XX
; DE Human MEKK4 antisense oligonucleotide, ISIS #123085.
; XX

```
; KW   Human; MEKK4 modulation; mitogen-activated protein kinase kinase 4; MTK1;
; KW   MAP3K4; MAP three kinase 1; MAP/ERK kinase kinase 4; MAPKKK4; cytostatic;
; KW   prophylaxis; immunological; hyperproliferative disorder; cancer; therapy;
; KW   antisense; inflammatory; phosphorothioate backbone; ss.
; XX
; OS   Homo sapiens.
; OS   Synthetic.
; XX
; FH   Key             Location/Qualifiers
; FT   modified_base   1. .20
; FT                   /*tag= a
; FT                   /mod_base= OTHER
; FT                   /note= "Phosphorothioate backbone"
; FT   modified_base   1. .5
; FT                   /*tag= b
; FT                   /mod_base= OTHER
; FT                   /note= "2'-methoxyethyl nucleotides"
; FT   modified_base   16. .20
; FT                   /*tag= c
; FT                   /mod_base= OTHER
; FT                   /note= "2'-methoxyethyl nucleotides"
; FT   modified_base   2
; FT                   /*tag= d
; FT                   /mod_base= m5c
; FT   modified_base   8
; FT                   /*tag= e
; FT                   /mod_base= m5c
; FT   modified_base   9
; FT                   /*tag= f
; FT                   /mod_base= m5c
; FT   modified_base   10
; FT                   /*tag= g
; FT                   /mod_base= m5c
; FT   modified_base   11
; FT                   /*tag= h
; FT                   /mod_base= m5c
; FT   modified_base   17
; FT                   /*tag= i
; FT                   /mod_base= m5c
; FT   modified_base   18
; FT                   /*tag= j
; FT                   /mod_base= m5c
; FT   modified_base   19
; FT                   /*tag= k
; FT                   /mod_base= m5c
; XX
; PN   WO200227033-A1.
; XX
; PD   04-APR-2002.
; XX
; PF   28-SEP-2001; 2001WO-US30549.
; XX
; PR   29-SEP-2000; 2000US-0676436.
; XX
; PA   (ISIS-) ISIS PHARM INC.
; XX
; PI   Ward DT, Gaarde WA, Monia BP, Wyatt JR;
; XX
; DR   WPI; 2002-416486/44.
; XX
; PT   New antisense compound targeted to nucleic acid encoding
; PT   mitogen-activated protein kinase 4, useful for treating immunologic
; PT   disorder, inflammatory disorder or cancer -
; XX
; PS   Claim 3; Page 92; 132pp; English.
; XX
; CC   The present invention relates to antisense compounds, compositions and
; CC   methods for modulating the expression of MEKK4 (also referred as mitogen-
; CC   activated protein kinase kinase 4; MAP3K4; MAP three kinase 1; MAP/ERK
; CC   kinase kinase 4; MAPKKK4; MTK1). The antisense oligos are useful for
; CC   inhibiting the expression of MEKK4 in cells or tissues. They are also
; CC   useful for treating an animal having a disease or condition associated
; CC   with MEKK4 such as immunological, inflammatory, hyperproliferative
; CC   disorder or cancer. Sequences of the invention are also useful for
; CC   diagnostics, therapeutics, prophylaxis and as research reagents and kits.
; CC   They are also useful in antisense therapy. The present sequence is an
; CC   antisense oligonucleotide targetted to human MEKK4 DNA. This sequence
; CC   is used in the exemplification of the invention.
; XX
; SQ   Sequence 20 BP; 4 A; 8 C; 4 G; 4 T; 0 other;
;
;  AAD37150  Length: 20  October 2, 2003 14:57  Type: N  Check: 4945  ..
aad37150

  Query Match             100.0%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0.11;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3314 AGGGATTCAGGGGTTCCAGC 3333
              ||||||||||||||||||||
Db         20 AGGGATTCAGGGGTTCCAGC 1


RESULT 2
aaq83338
;  TOIG of: aaq83338  check: 7525  from: 1  to: 14
;
; ID   AAQ83338 standard; DNA; 14 BP.
; XX
; AC   AAQ83338;
; XX
; DT   25-MAR-2003  (updated)
; DT   20-SEP-1995  (first entry)
; XX
; DE   jub-B antisense oligonucleotide.
; XX
; KW   c-jun; c-fos; jun-B; neuronal injury; cell death; neoplasm;
; KW   antisense; phosphorothioate; ss.
; XX
; OS   Synthetic.
; XX
; PN   WO9502051-A2.
; XX
; PD   19-JAN-1995.
; XX
; PF   06-JUL-1994;   94WO-EP02218.
; XX
; PR   10-JUL-1993;   93EP-0111059.
; XX
; PA   (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
; XX
; PI   Brysch W, Schlingensiepen G, Schlingensiepen K, Schlingensiepen R;
; XX
; DR   WPI; 1995-066896/09.
; XX
; PT   Use of antisense c-jun, c-fos or jun-B nucleic acids - for
; PT   preventing and treating neuronal injury, degeneration, cell death
; PT   and/or neoplasms
; XX
; PS   Claim 2; Page 40; 86pp; English.
; XX
; CC   Antisense nucleic acid hybridising with an area of the mRNA and/or
; CC   DNA comprising the genes c-jun, jun-B or c-fos, expression of which
; CC   plays a causal role in neuronal injury, degeneration, cell death and/
; CC   or neoplasms, can be used to prevent and treat such conditions.
; CC   c-jun antisense sequences are described in AAQ83267-321 and AAQ83440-43;
; CC   jun-B antisense sequences are described in AAQ83322-63 and AAQ83444-45;
; CC   and c-fos antisense sequences are described in AAQ83364-439 and
; CC   AAQ83446- 51.  Preferably the antisense sequences are phosphorothioate
; CC   oligonucleotides since these are not destroyed as fast by endogenous
; CC   factors as naturally occuring molecules.
; CC   (Updated on 25-MAR-2003 to correct PN field.)
; XX
; SQ   Sequence 14 BP; 3 A; 4 C; 3 G; 4 T; 0 other;
;
;  AAQ83338  Length: 14  October 2, 2003 14:57  Type: N  Check: 7525  ..
```

```
aaq83338

  Query Match             62.0%;  Score 12.4;  DB 1;  Length 14;
  Best Local Similarity   92.9%;  Pred. No. 4.2;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3318 ATTCAGGGGTTCCA 3331
              ||||||| ||||||
Db          1 ATTCAGGCGTTCCA 14


RESULT 3
abq87435/c
;  TOIG of: abq87435  check: 4620  from: 1  to: 11
;
; ID   ABQ87435 standard; cDNA; 11 BP.
; XX
; AC   ABQ87435;
; XX
; DT   10-SEP-2002  (first entry)
; XX
; DE   Human skin stress/ageing related EST SEQ ID NO 1190.
; XX
; KW   Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   WO200253773-A2.
; XX
; PD   11-JUL-2002.
; XX
; PF   20-DEC-2001; 2001WO-EP15178.
; XX
; PR   03-JAN-2001; 2001DE-1000121.
; XX
; PA   (HENK ) HENKEL KGAA.
; XX
; PI   Petersohn D,  Conradt M,  Hofmann K;
; XX
; DR   WPI; 2002-528865/56.
; XX
; PT   Identifying genes involved in skin stress and ageing, useful e.g. in
; PT   screening for cosmetic or therapeutic agents, based on differential
; PT   gene expression  -
; XX
; PS   Claim 8; Page 86; 325pp; German.
; XX
; CC   The invention relates to identifying (M1) genes in vitro that, in humans
; CC   or animals, are important for skin ageing and/or skin stress by serial
; CC   analysis of gene expression between mixtures of transcribed and
; CC   optionally translated, genetically encoded factors (A) obtained from
; CC   young and aged skin, to identify that genes that show strong differential
; CC   expression. (A) comprises protein or mRNAs or their fragments. (M1) is
; CC   useful for: identifying markers of skin ageing and/or stress; determining
; CC   skin ageing and/or stress; and identifying or determining the effects of
; CC   pharmaceutical or cosmetic agents for control of skin ageing. The present
; CC   sequence is one of a group of human skin ageing/stress related expressed
; CC   sequence tags (ABQ86246-ABQ87680) of the invention.
; XX
; SQ   Sequence 11 BP; 2 A; 6 C; 1 G; 2 T; 0 other;
;
;  ABQ87435  Length: 11  October 2, 2003 14:57  Type: N  Check: 4620  ..
abq87435

  Query Match             55.0%;  Score 11;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 9.6;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3315 GGGATTCAGGG 3325
              ||||||||||
Db         11 GGGATTCAGGG 1


RESULT 4
abv67711/c
;  TOIG of: abv67711  check: 4620  from: 1  to: 11
;
; ID   ABV67711 standard; cDNA; 11 BP.
; XX
; AC   ABV67711;
; XX
; DT   21-OCT-2002  (first entry)
; XX
; DE   Human skin EST 5497.
; XX
; KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
; KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
; KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   WO200253774-A2.
; XX
; PD   11-JUL-2002.
; XX
; PF   20-DEC-2001; 2001WO-EP15179.
; XX
; PR   03-JAN-2001; 2001DE-1000127.
; XX
; PA   (HENK ) HENKEL KGAA.
; XX
; PI   Petersohn D,  Conradt M,  Hofmann K;
; XX
; DR   WPI; 2002-590638/63.
; XX
; PT   In vitro identification of skin-expressed genes, useful for determining
; PT   homeostasis and identifying cosmetic or pharmaceutical agents against
; PT   e.g. skin cancer  -
; XX
; PS   Disclosure; Page 177; 1345pp; German.
; XX
; CC   The invention relates to in vitro identification (M1) of genes expressed
; CC   in the skin of humans or animals by subjecting a mixture of genetically
; CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
; CC   so as to identify skin-expressed genes and quantify their expression.
; CC   (M1) is useful for identifying genes involved in skin homeostasis; to
; CC   determine skin homeostasis and to test agent (A) that maintains or
; CC   promotes skin homeostasis or that can be used for treating skin
; CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
; CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
; CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
; CC   skin. The present sequence is that of a human expressed sequence tag
; CC   (EST) of the invention.
; XX
; SQ   Sequence 11 BP; 2 A; 6 C; 1 G; 2 T; 0 other;
;
;  ABV67711  Length: 11  October 2, 2003 14:57  Type: N  Check: 4620  ..
abv67711

  Query Match             55.0%;  Score 11;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 9.6;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3315 GGGATTCAGGG 3325
              ||||||||||
Db         11 GGGATTCAGGG 1


RESULT 5
aaz83859/c
;  TOIG of: aaz83859  check: 3883  from: 1  to: 10
;
; ID   AAZ83859 standard; DNA; 10 BP.
; XX
; AC   AAZ83859;
; XX
```

```
; DT   07-APR-2000  (first entry)
; XX
; DE   Metastatic breast tumour cell upregulated transcript tag #3093.
; XX
; KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
; KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
; KW   antimetastatic; vaccine; diagnosis; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   WO9965928-A2.
; XX
; PD   23-DEC-1999.
; XX
; PF   18-JUN-1999;   99WO-US13647.
; XX
; PR   19-JUN-1998;   98US-0089853.
; PR   19-JUN-1998;   98US-0089997.
; PR   19-JUN-1998;   98US-0090039.
; PR   19-JUN-1998;   98US-0090040.
; PR   19-JUN-1998;   98US-0090041.
; XX
; PA   (GENZ ) GENZYME CORP.
; PA   (ROBE/) ROBERTS B L.
; PA   (SHAN/) SHANKARA S.
; XX
; PI   Roberts BL,  Shankara S;
; XX
; DR   WPI; 2000-106079/09.
; XX
; PT   Isolated polynucleotides differentially expressed between metastatic
; PT   and non-metastatic breast cancer cells, useful for diagnosis,
; PT   prevention and treatment of cancer -
; XX
; PS   Claim 1; Page 141; 219pp; English.
; XX
; CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
; CC   transcripts that are preferentially transcribed in the metastatic breast
; CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
; CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
; CC   that are preferentially transcribed in the primary or non-metastatic
; CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
; CC   cells). These transcripts can be used for diagnosis, prognosis,
; CC   monitoring and treatment of breast cancer, particularly where metastatic.
; CC   Diagnosis is by standard immunoassays or hybridisation/amplification
; CC   reactions. Compounds that modulate expression of the transcripts are
; CC   potentially useful for treatment of (metastatic) breast cancer, while
; CC   promoters from the transcripts are used to direct expression, in selected
; CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
; CC   sequences), particularly an antigen-encoding sequence for use in gene or
; CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
; CC   useful in vaccines; for diagnosing breast cancer and for raising
; CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
; CC   therapeutic agents. Host cells that produce the polypeptides can be used
; CC   to expand and isolate populations of educated, antigen-specific immune
; CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
; CC   adoptive immunotherapy.
; XX
; SQ   Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 other;
;
;  AAZ83859  Length: 10  October 2, 2003 14:57  Type: N  Check: 3883  ..
aaz83859

  Query Match             50.0%;  Score 10;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 16;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3316 GGATTCAGGG 3325
              ||||||||||
Db         10 GGATTCAGGG 1


RESULT 6
```

```
abv66038/c
;  TOIG of: abv66038  check: 4483  from: 1  to: 11
;
; ID   ABV66038 standard; cDNA; 11 BP.
; XX
; AC   ABV66038;
; XX
; DT   21-OCT-2002  (first entry)
; XX
; DE   Human skin EST 3824.
; XX
; KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
; KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
; KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   WO200253774-A2.
; XX
; PD   11-JUL-2002.
; XX
; PF   20-DEC-2001; 2001WO-EP15179.
; XX
; PR   03-JAN-2001; 2001DE-1000127.
; XX
; PA   (HENK ) HENKEL KGAA.
; XX
; PI   Petersohn D,  Conradt M,  Hofmann K;
; XX
; DR   WPI; 2002-590638/63.
; XX
; PT   In vitro identification of skin-expressed genes, useful for determining
; PT   homeostasis and identifying cosmetic or pharmaceutical agents against
; PT   e.g. skin cancer  -
; XX
; PS   Disclosure; Page 131; 1345pp; German.
; XX
; CC   The invention relates to in vitro identification (M1) of genes expressed
; CC   in the skin of humans or animals by subjecting a mixture of genetically
; CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
; CC   so as to identify skin-expressed genes and quantify their expression.
; CC   (M1) is useful for identifying genes involved in skin homeostasis; to
; CC   determine skin homeostasis and to test agent (A) that maintains or
; CC   promotes skin homeostasis or that can be used for treating skin
; CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
; CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
; CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
; CC   skin. The present sequence is that of a human expressed sequence tag
; CC   (EST) of the invention.
; XX
; SQ   Sequence 11 BP; 2 A; 6 C; 2 G; 1 T; 0 other;
;
;  ABV66038  Length: 11  October 2, 2003 14:57  Type: N  Check: 4483  ..
abv66038

  Query Match             50.0%;  Score 10;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3323 GGGGTTCCAG 3332
              ||||||||||
Db         11 GGGGTTCCAG 2


RESULT 7
aal42209/c
;  TOIG of: aal42209  check: 4662  from: 1  to: 11
;
; ID   AAL42209 standard; RNA; 11 BP.
; XX
; AC   AAL42209;
; XX
; DT   28-NOV-2002  (first entry)
```

```
; XX
; DE   Saccharomyces cerevisiae U3 small nucleolar RNA (snoRNA) 3' hinge region.
; XX
; KW   U3 snoRNA 3' hinge region; ss; antibiotic agent screening; yeast;
; KW   U3 small nucleolar RNA domain I hinge region; snoRNA; pre-rRNA;
; KW   18S rRNA subunit; cell growth inhibition; fungal infection;
; KW   protozoa infection; Chagas disease; Trypanosoma cruzi infection;
; KW   Pneumocystis carinii infection; coccidiosis; Eimeria infection.
; XX
; OS   Saccharomyces cerevisiae.
; XX
; PN   WO200201953-A1.
; XX
; PD   10-JAN-2002.
; XX
; PF   28-JUN-2001; 2001WO-US20520.
; XX
; PR   30-JUN-2000; 2000US-215572P.
; XX
; PA   (UYBR-) UNIV BROWN RES FOUND.
; XX
; PI   Gerbi S,  Borovjagin A,  Lange TS;
; XX
; DR   WPI; 2002-154668/20.
; XX
; PT   Identification of antibiotic agents, useful to treat opportunist
; PT   infections in humans and domestic animals, comprises disrupting binding
; PT   of specific regions of U3 small nucleolar ribonucleic acid to
; PT   complementary sequences in pre-rRNA  -
; XX
; PS   Disclosure; Page 18; 74pp; English.
; XX
; CC   The invention comprises a method of screening for antibiotic agents. The
; CC   method involves disrupting binding of the 5' and 3' hinge regions of
; CC   domain I of U3 small nucleolar RNA (snoRNA) to complementary sequences in
; CC   the ribosomal RNA precursor (pre-rRNA). Thereby preventing processing of
; CC   the pre-rRNA into a functional 18S rRNA subunit of the cellular
; CC   translation machinery. The method of the invention is useful in screening
; CC   for antibiotics which can be used to inhibit cell growth of infectious
; CC   organisms and/or treat opportunistic infections in eukaryotic hosts (i.e.
; CC   humans and domestic animals). The antibiotics identified by the method of
; CC   the invention may be used to treat opportunistic infections in humans
; CC   (e.g. fungi, protozoa and multicellular parasites, Chagas disease caused
; CC   by Trypanosoma cruzi, and Pneumocystis carinii infections in
; CC   immunocompromised hosts). The antibodies identified by the method of the
; CC   invention may also be used to treat infections in domesticated animals
; CC   (e.g. coccidiosis in poultry caused by infection with Eimeria). The
; CC   present RNA sequence represents the Saccharomyces cerevisiae U3 snoRNA 3'
; CC   hinge region.
; XX
; SQ   Sequence 11 BP; 3 A; 5 C; 1 G; 2 U; 0 other;
;
;  AAL42209  Length: 11  October 2, 2003 14:57  Type: N  Check: 4662  ..
aal42209

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 18;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3316 GGATTCAGGGG 3326
             |||||||| ||
Db         11 GGATTCAGTGG 1


RESULT 8
abq86371/c
;  TOIG of: abq86371  check: 4600  from: 1  to: 11
;
; ID   ABQ86371 standard; cDNA; 11 BP.
; XX
; AC   ABQ86371;
; XX
; DT   10-SEP-2002  (first entry)
; XX
; DE   Human skin stress/ageing related EST SEQ ID NO 126.
; XX
; KW   Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   WO200253773-A2.
; XX
; PD   11-JUL-2002.
; XX
; PF   20-DEC-2001; 2001WO-EP15178.
; XX
; PR   03-JAN-2001; 2001DE-1000121.
; XX
; PA   (HENK ) HENKEL KGAA.
; XX
; PI   Petersohn D,  Conradt M,  Hofmann K;
; XX
; DR   WPI; 2002-528865/56.
; XX
; PT   Identifying genes involved in skin stress and ageing, useful e.g. in
; PT   screening for cosmetic or therapeutic agents, based on differential
; PT   gene expression  -
; XX
; PS   Claim 8; Page 42; 325pp; German.
; XX
; CC   The invention relates to identifying (M1) genes in vitro that, in humans
; CC   or animals, are important for skin ageing and/or skin stress by serial
; CC   analysis of gene expression between mixtures of transcribed and
; CC   optionally translated, genetically encoded factors (A) obtained from
; CC   young and aged skin, to identify that genes that show strong differential
; CC   expression. (A) comprises protein or mRNAs or their fragments. (M1) is
; CC   useful for: identifying markers of skin ageing and/or stress; determining
; CC   skin ageing and/or stress; and identifying or determining the effects of
; CC   pharmaceutical or cosmetic agents for control of skin ageing. The present
; CC   sequence is one of a group of human skin ageing/stress related expressed
; CC   sequence tags (ABQ86246-ABQ87680) of the invention.
; XX
; SQ   Sequence 11 BP; 2 A; 7 C; 0 G; 2 T; 0 other;
;
;  ABQ86371  Length: 11  October 2, 2003 14:57  Type: N  Check: 4600  ..
abq86371

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 18;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3315 GGGATTCAGGG 3325
             |||||| ||||
Db         11 GGGATTGAGGG 1


RESULT 9
abv62683/c
;  TOIG of: abv62683  check: 4600  from: 1  to: 11
;
; ID   ABV62683 standard; cDNA; 11 BP.
; XX
; AC   ABV62683;
; XX
; DT   21-OCT-2002  (first entry)
; XX
; DE   Human skin EST 469.
; XX
; KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
; KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
; KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   WO200253774-A2.
; XX
```

```
; PD   11-JUL-2002.
; XX
; PF   20-DEC-2001; 2001WO-EP15179.
; XX
; PR   03-JAN-2001; 2001DE-1000127.
; XX
; PA   (HENK ) HENKEL KGAA.
; XX
; PI   Petersohn D,  Conradt M,  Hofmann K;
; XX
; DR   WPI; 2002-590638/63.
; XX
; PT   In vitro identification of skin-expressed genes, useful for determining
; PT   homeostasis and identifying cosmetic or pharmaceutical agents against
; PT   e.g. skin cancer  -
; XX
; PS   Disclosure; Page 38; 1345pp; German.
; XX
; CC   The invention relates to in vitro identification (M1) of genes expressed
; CC   in the skin of humans or animals by subjecting a mixture of genetically
; CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
; CC   so as to identify skin-expressed genes and quantify their expression.
; CC   (M1) is useful for identifying genes involved in skin homeostasis; to
; CC   determine skin homeostasis and to test agent (A) that maintains or
; CC   promotes skin homeostasis or that can be used for treating skin
; CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
; CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
; CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
; CC   skin. The present sequence is that of a human expressed sequence tag
; CC   (EST) of the invention.
; XX
; SQ   Sequence 11 BP; 2 A; 7 C; 0 G; 2 T; 0 other;
;
;  ABV62683  Length: 11  October 2, 2003 14:57  Type: N  Check: 4600  ..
abv62683

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 18;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3315 GGGATTCAGGG 3325
             |||||| ||||
Db         11 GGGATTGAGGG 1


RESULT 10
abv68833
;  TOIG of: abv68833  check: 4860  from: 1  to: 11
;
; ID   ABV68833 standard; cDNA; 11 BP.
; XX
; AC   ABV68833;
; XX
; DT   21-OCT-2002  (first entry)
; XX
; DE   Human skin EST 6619.
; XX
; KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
; KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
; KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   WO200253774-A2.
; XX
; PD   11-JUL-2002.
; XX
; PF   20-DEC-2001; 2001WO-EP15179.
; XX
; PR   03-JAN-2001; 2001DE-1000127.
; XX
; PA   (HENK ) HENKEL KGAA.
; XX
; PI   Petersohn D,  Conradt M,  Hofmann K;
; XX
; DR   WPI; 2002-590638/63.
; XX
; PT   In vitro identification of skin-expressed genes, useful for determining
; PT   homeostasis and identifying cosmetic or pharmaceutical agents against
; PT   e.g. skin cancer  -
; XX
; PS   Disclosure; Page 209; 1345pp; German.
; XX
; CC   The invention relates to in vitro identification (M1) of genes expressed
; CC   in the skin of humans or animals by subjecting a mixture of genetically
; CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
; CC   so as to identify skin-expressed genes and quantify their expression.
; CC   (M1) is useful for identifying genes involved in skin homeostasis; to
; CC   determine skin homeostasis and to test agent (A) that maintains or
; CC   promotes skin homeostasis or that can be used for treating skin
; CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
; CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
; CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
; CC   skin. The present sequence is that of a human expressed sequence tag
; CC   (EST) of the invention.
; XX
; SQ   Sequence 11 BP; 1 A; 3 C; 3 G; 4 T; 0 other;
;
;  ABV68833  Length: 11  October 2, 2003 14:57  Type: N  Check: 4860  ..
abv68833

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 18;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3319 TTCAGGGGTTC 3329
             ||||||| |||
Db         1 TTCAGGGCTTC 11


RESULT 11
abv70104/c
;  TOIG of: abv70104  check: 4600  from: 1  to: 11
;
; ID   ABV70104 standard; cDNA; 11 BP.
; XX
; AC   ABV70104;
; XX
; DT   21-OCT-2002  (first entry)
; XX
; DE   Human skin EST 7890.
; XX
; KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
; KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
; KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   WO200253774-A2.
; XX
; PD   11-JUL-2002.
; XX
; PF   20-DEC-2001; 2001WO-EP15179.
; XX
; PR   03-JAN-2001; 2001DE-1000127.
; XX
; PA   (HENK ) HENKEL KGAA.
; XX
; PI   Petersohn D,  Conradt M,  Hofmann K;
; XX
; DR   WPI; 2002-590638/63.
; XX
; PT   In vitro identification of skin-expressed genes, useful for determining
; PT   homeostasis and identifying cosmetic or pharmaceutical agents against
; PT   e.g. skin cancer  -
; XX
```

; PS Claim 24; Page 251; 1345pp; German.
; XX
; CC The invention relates to in vitro identification (M1) of genes expressed
; CC in the skin of humans or animals by subjecting a mixture of genetically
; CC encoded factors from skin, to serial analysis of gene expression (SAGE)
; CC so as to identify skin-expressed genes and quantify their expression.
; CC (M1) is useful for identifying genes involved in skin homeostasis; to
; CC determine skin homeostasis and to test agent (A) that maintains or
; CC promotes skin homeostasis or that can be used for treating skin
; CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
; CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
; CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
; CC skin. The present sequence is that of a human expressed sequence tag
; CC (EST) of the invention.
; XX
; SQ Sequence 11 BP; 2 A; 7 C; 0 G; 2 T; 0 other;
;
; ABV70104 Length: 11 October 2, 2003 14:57 Type: N Check: 4600 ..
abv70104

Query Match 47.0%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 18;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3315 GGGATTCAGGG 3325
|||||| ||||
Db 11 GGGATTGAGGG 1

RESULT 12
aac74212
; TOIG of: aac74212 check: 4052 from: 1 to: 10
;
; ID AAC74212 standard; cDNA; 10 BP.
; XX
; AC AAC74212;
; XX
; DT 02-FEB-2001 (first entry)
; XX
; DE Human monocyte and dendritic cell expressed gene oligonucleotide #299.
; XX
; KW Human; dendritic cell; monocyte; immune system; diagnosis; cancer;
; KW autoimmune disease; tumour; ss.
; XX
; OS Homo sapiens.
; XX
; PN WO200060074-A1.
; XX
; PD 12-OCT-2000.
; XX
; PF 30-MAR-2000; 2000WO-JP02019.
; XX
; PR 01-APR-1999; 99JP-0095481.
; XX
; PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
; XX
; PI Hashimoto S, Matsushima K, Suzuki T;
; XX
; DR WPI; 2000-619172/59.
; XX
; PT Groups of genes expressed in human dendritic cells at a greater or
; PT lesser extent than in monocytes for investigation and diagnosis of
; PT autoimmune disease and tumors -
; XX
; PS Claim 19; Page 16; 95pp; Japanese.
; XX
; CC The present invention describes a group of genes consisting of 100 genes
; CC which are highly expressed in human dendritic cells; a group of genes
; CC which are expressed at a higher frequency in human dendritic cells than
; CC in human monocytes; and a group of genes which are expressed at lower
; CC frequency in human dendritic cells than in human monocytes. Each group
; CC of genes are characterised in that cDNAs of these genes respectively
; CC have the base sequences of SEQ ID NO:1 to 100 (AAC73914 to AAC74013),
; CC SEQ ID NO:101 to 200 (AAC74014 to AAC74113) and SEQ ID NO:201 to 300
; CC (AAC74114 to AAC74213), each is continuous with the base sequence
; CC 5'-CATG-3' located most closely to the poly-A region. The sequences can
; CC be used for the investigation of the role and mechanism of the
; CC involvement of dendritic cells in the immune system and for the study and
; CC diagnosis of diseases in which dendritic cells play a significant role,
; CC e.g. cancers and autoimmune diseases.
; XX
; SQ Sequence 10 BP; 1 A; 2 C; 4 G; 3 T; 0 other;
;
; AAC74212 Length: 10 October 2, 2003 14:57 Type: N Check: 4052 ..
aac74212

Query Match 45.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3324 GGGTTCCAG 3332
||||||||| |
Db 1 GGGTTCCAG 9

RESULT 13
aaf42053
; TOIG of: aaf42053 check: 3956 from: 1 to: 10
;
; ID AAF42053 standard; DNA; 10 BP.
; XX
; AC AAF42053;
; XX
; DT 23-MAR-2001 (first entry)
; XX
; DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8792.
; XX
; KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
; KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
; KW serial analysis of gene expression; antifungal; tag; identification;
; KW linker; PCR primer; ds.
; XX
; OS Saccharomyces cerevisiae.
; XX
; PN WO200077214-A2.
; XX
; PD 21-DEC-2000.
; XX
; PF 14-JUN-2000; 2000WO-US16223.
; XX
; PR 16-JUN-1999; 99US-0335032.
; XX
; PA (UYJO) UNIV JOHNS HOPKINS.
; XX
; PI Velculescu V, Vogelstein B, Kinzler K;
; XX
; DR WPI; 2001-061874/07.
; XX
; PT Yeast gene coding sequences comprising NORF genes with serial analysis
; PT of gene expression (SAGE) tags, useful for studying, monitoring and
; PT affecting phases of the cell cycle -
; XX
; PS Example; Page 314; 419pp; English.
; XX
; CC The present invention describes an isolated DNA molecule comprising a
; CC coding sequence of a yeast gene selected from a group of 745 NORF (not
; CC previously assigned open reading frame; or nonannotated ORF) genes
; CC comprising a SAGE (serial analysis of gene expression) tag. Also
; CC described are: (1) a method (M1) of using NORF genes to affect the cell
; CC cycle comprising administering a NORF gene whose expression varies by at
; CC least 10% between any two phases of the cell cycle selected from log
; CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
; CC antifungal drugs comprising: (a) contacting a test substance with a
; CC yeast cell; and (b) monitoring expression of a NORF gene whose
; CC expression varies as in M1, where a test substance which modifies the
; CC expression of the yeast gene is a candidate antifungal drug; (3) a method

```
; CC   (M3) for identifying human genes which are involved in cell cycle
; CC   progression comprising contacting human DNA with a probe which comprises
; CC   at least 10 contiguous nucleotides of a NORF gene whose expression varies
; CC   as in M1; and (4) a method (M4) for identifying a candidate drug as a
; CC   member of a class of drugs having a characteristic effect on gene
; CC   expression in a yeast cell comprising contacting a yeast cell with a
; CC   candidate drug and monitoring expression in the yeast cell of at least 1
; CC   NORF gene whose expression is affected by the class of drugs. The NORF
; CC   genes may be used to study, monitor and affect phases of the cell cycle,
; CC   the differentially expressed genes may be used as markers of phases of
; CC   the cell cycle. The methods may be used to identify candidate drugs which
; CC   affect the cell cycle and for identification of antifungal drugs.
; CC   AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
; CC   the present invention. AAF33262 to AAF33267 represent linkers and PCR
; CC   primers used in the SAGE method, in the exemplification of the present
; CC   invention.
; XX
; SQ   Sequence 10 BP; 3 A; 1 C; 4 G; 2 T; 0 other;
;
;  AAF42053  Length: 10  October 2, 2003 14:57  Type: N  Check: 3956  ..
aaf42053

  Query Match             45.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 24;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3314 AGGGATTCA 3322
              |||||||||
Db          2 AGGGATTCA 10


RESULT 14
aal48142/c
;  TOIG of: aal48142  check: 3815  from: 1  to: 10
;
; ID   AAL48142 standard; DNA; 10 BP.
; XX
; AC   AAL48142;
; XX
; DT   27-SEP-2002  (first entry)
; XX
; DE   Human neuropeptide Y primer extension oligo SEQ ID NO: 66.
; XX
; KW   Human; neuropeptide Y; NPY; isogene; SNP; atherosclerosis; obesity;
; KW   psychological disorder; single nucleotide polymorphism; alcoholism;
; KW   antiarteriosclerotic; anorectic; PCR; primer extension oligonucleotide;
; KW   ss.
; XX
; OS   Homo sapiens.
; XX
; PN   WO200251857-A1.
; XX
; PD   04-JUL-2002.
; XX
; PF   21-DEC-2000; 2000WO-US34758.
; XX
; PR   21-DEC-2000; 2000WO-US34758.
; XX
; PA   (GENA-) GENAISSANCE PHARM INC.
; XX
; PI   Chew A,  Denton RR,  Lanz EM,  Nandabalan K,  Stephens JC;
; XX
; DR   WPI; 2002-566671/60.
; XX
; PT   New genetic variants of the human Neuropeptide Y (NPY) gene useful for
; PT   treating disorders affected by abnormal expression or function of NPY
; PT   isogene e.g., atherosclerosis or obesity -
; XX
; PS   Disclosure; Page 17; 80pp; English.
; XX
; CC   The present invention provides the human neuropeptide Y (NPY) gene and
; CC   single nucleotide polymorphisms (SNPs) identified therein. The sequence
; CC   can be used in the treatment of disorders associated with NPY, including
; CC   atherosclerosis, obesity, psychological disorders and alcoholism. The
; CC   present sequence is an allele specific primer extension oligonucleotide
; CC   used to isolate the human NPY coding sequence.
; XX
; SQ   Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 other;
;
;  AAL48142  Length: 10  October 2, 2003 14:57  Type: N  Check: 3815  ..
aal48142

  Query Match             45.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 24;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3315 GGGATTCAG 3323
              |||||||||
Db          9 GGGATTCAG 1


RESULT 15
aaz83465/c
;  TOIG of: aaz83465  check: 3729  from: 1  to: 10
;
; ID   AAZ83465 standard; DNA; 10 BP.
; XX
; AC   AAZ83465;
; XX
; DT   07-APR-2000  (first entry)
; XX
; DE   Metastatic breast tumour cell upregulated transcript tag #2699.
; XX
; KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
; KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
; KW   antimetastatic; vaccine; diagnosis; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   WO9965928-A2.
; XX
; PD   23-DEC-1999.
; XX
; PF   18-JUN-1999;   99WO-US13647.
; XX
; PR   19-JUN-1998;   98US-0089853.
; PR   19-JUN-1998;   98US-0089997.
; PR   19-JUN-1998;   98US-0090039.
; PR   19-JUN-1998;   98US-0090040.
; PR   19-JUN-1998;   98US-0090041.
; XX
; PA   (GENZ ) GENZYME CORP.
; PA   (ROBE/) ROBERTS B L.
; PA   (SHAN/) SHANKARA S.
; XX
; PI   Roberts BL,  Shankara S;
; XX
; DR   WPI; 2000-106079/09.
; XX
; PT   Isolated polynucleotides differentially expressed between metastatic
; PT   and non-metastatic breast cancer cells, useful for diagnosis,
; PT   prevention and treatment of cancer -
; XX
; PS   Claim 1; Page 131; 219pp; English.
; XX
; CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
; CC   transcripts that are preferentially transcribed in the metastatic breast
; CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
; CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
; CC   that are preferentially transcribed in the primary or non-metastatic
; CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
; CC   cells). These transcripts can be used for diagnosis, prognosis,
; CC   monitoring and treatment of breast cancer, particularly where metastatic.
; CC   Diagnosis is by standard immunoassays or hybridisation/amplification
; CC   reactions. Compounds that modulate expression of the transcripts are
; CC   potentially useful for treatment of (metastatic) breast cancer, while
```

; CC promoters from the transcripts are used to direct expression, in selected
; CC cell types, of e.g. therapeutic genes (also ribozymes or antisense
; CC sequences), particularly an antigen-encoding sequence for use in gene or
; CC cell-based vaccines. Polypeptides encoded by the transcripts are also
; CC useful in vaccines; for diagnosing breast cancer and for raising
; CC specific antibodies (Ab). Ab are used to detect the polypeptides or as
; CC therapeutic agents. Host cells that produce the polypeptides can be used
; CC to expand and isolate populations of educated, antigen-specific immune
; CC effecter cells, e.g. cytotoxic T lymphocytes, and these used for
; CC adoptive immunotherapy.
; XX
; SQ Sequence 10 BP; 2 A; 4 C; 3 G; 1 T; 0 other;
;
; AAZ83465 Length: 10 October 2, 2003 14:57 Type: N Check: 3729 ..
aaz83465

Query Match 45.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3323 GGGGTTCCA 3331
||||||||| |
Db 10 GGGGTTCCA 2

RESULT 16
aaz84256
; TOIG of: aaz84256 check: 4054 from: 1 to: 10
;
; ID AAZ84256 standard; DNA; 10 BP.
; XX
; AC AAZ84256;
; XX
; DT 07-APR-2000 (first entry)
; XX
; DE Metastatic breast tumour cell downregulated transcript tag #3490.
; XX
; KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
; KW non-metastatic breast tumour tissue; gene therapy; anticancer;
; KW antimetastatic; vaccine; diagnosis; ss.
; XX
; OS Homo sapiens.
; XX
; PN WO9965928-A2.
; XX
; PD 23-DEC-1999.
; XX
; PF 18-JUN-1999; 99WO-US13647.
; XX
; PR 19-JUN-1998; 98US-0089853.
; PR 19-JUN-1998; 98US-0089997.
; PR 19-JUN-1998; 98US-0090039.
; PR 19-JUN-1998; 98US-0090040.
; PR 19-JUN-1998; 98US-0090041.
; XX
; PA (GENZ) GENZYME CORP.
; PA (ROBE/) ROBERTS B L.
; PA (SHAN/) SHANKARA S.
; XX
; PI Roberts BL, Shankara S;
; XX
; DR WPI; 2000-106079/09.
; XX
; PT Isolated polynucleotides differentially expressed between metastatic
; PT and non-metastatic breast cancer cells, useful for diagnosis,
; PT prevention and treatment of cancer -
; XX
; PS Claim 1; Page 152; 219pp; English.
; XX
; CC AAZ80767 to AAZ83941 represent tags corresponding to distinct
; CC transcripts that are preferentially transcribed in the metastatic breast
; CC tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
; CC AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
; CC that are preferentially transcribed in the primary or non-metastatic
; CC breast tumour tissue (i.e. are downregulated in metastatic breast tumour
; CC cells). These transcripts can be used for diagnosis, prognosis,
; CC monitoring and treatment of breast cancer, particularly where metastatic.
; CC Diagnosis is by standard immunoassays or hybridisation/amplification
; CC reactions. Compounds that modulate expression of the transcripts are
; CC potentially useful for treatment of (metastatic) breast cancer, while
; CC promoters from the transcripts are used to direct expression, in selected
; CC cell types, of e.g. therapeutic genes (also ribozymes or antisense
; CC sequences), particularly an antigen-encoding sequence for use in gene or
; CC cell-based vaccines. Polypeptides encoded by the transcripts are also
; CC useful in vaccines; for diagnosing breast cancer and for raising
; CC specific antibodies (Ab). Ab are used to detect the polypeptides or as
; CC therapeutic agents. Host cells that produce the polypeptides can be used
; CC to expand and isolate populations of educated, antigen-specific immune
; CC effecter cells, e.g. cytotoxic T lymphocytes, and these used for
; CC adoptive immunotherapy.
; XX
; SQ Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 other;
;
; AAZ84256 Length: 10 October 2, 2003 14:57 Type: N Check: 4054 ..
aaz84256

Query Match 45.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3321 CAGGGGTTC 3329
||||||||| |
Db 2 CAGGGGTTC 10

RESULT 17
abk64082/c
; TOIG of: abk64082 check: 3790 from: 1 to: 10
;
; ID ABK64082 standard; DNA; 10 BP.
; XX
; AC ABK64082;
; XX
; DT 18-JUN-2002 (first entry)
; XX
; DE Human BF gene allele-specific oligonucleotide PCR primer #33.
; XX
; KW Human; B-factor; properdin; BF; primer; ss; gene therapy; drug screening;
; KW antidiabetic; dermatological; diabetes; immunosuppressive;
; KW antiinflammatory; systemic lupus erythematosus.
; XX
; OS Homo sapiens.
; XX
; PN WO200218414-A2.
; XX
; PD 07-MAR-2002.
; XX
; PF 29-AUG-2001; 2001WO-US27098.
; XX
; PR 29-AUG-2000; 2000US-228940P.
; XX
; PA (GENA-) GENAISSANCE PHARM INC.
; XX
; PI Anastasio AE, Finkel K, Kazemi A, Koshy B;
; XX
; DR WPI; 2002-304244/34.
; XX
; PT New genetic variants having polymorphisms in the B-Factor, Properdin
; PT (BF) gene, useful for studying the function of BF, and for treating
; PT disorders affected by expression or function of the BF isogene -
; XX
; PS Claim 19; Page 16; 151pp; English.
; XX
; CC The invention relates to single nucleotide polymorphisms in the gene
; CC encoding the human B-factor properdin protein (BF). A method for
; CC haplotyping the BF gene in an individual comprises identifying the

```
; CC   nucleotide at one or more polymorphic sites and determining whether one
; CC   of the copies of the gene is defined by one of the BF haplotypes given in
; CC   the specification or whether both copies are defined by a haplotype pair.
; CC   This method is useful in genotyping, whereby all possible haplotype pairs
; CC   can be assigned to specific genotypes. An association between a trait and
; CC   a haplotype or haplotype pair of the BF gene can be identified by
; CC   comparing the frequency of the haplotype or haplotype pair in a
; CC   population exhibiting the trait with the frequency of the haplotype or
; CC   haplotype pair in a reference population, where a higher haplotype
; CC   frequency in the trait population indicates the trait is associated with
; CC   the haplotype or haplotype pair. BF and its corresponding DNA are used
; CC   for studying the expression and function of BF, for use in screening for
; CC   candidate drugs to treat diseases related to BF activity, such as
; CC   diabetes and systemic lupus erythematosus. Sequences ABK64050-ABK64105
; CC   represent allele-specific PCR primers used to detect human BF gene
; CC   polymorphisms.
; XX
; SQ   Sequence 10 BP; 2 A; 3 C; 4 G; 1 T; 0 other;
;
;  ABK64082  Length: 10  October 2, 2003 14:57  Type: N  Check: 3790  ..
abk64082

  Query Match             45.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 24;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3325 GGTTCCAGC 3333
              |||||||||
Db          9 GGTTCCAGC 1


RESULT 18
aaf30844/c
;  TOIG of: aaf30844  check: 4634  from: 1  to: 11
;
; ID   AAF30844 standard; RNA; 11 BP.
; XX
; AC   AAF30844;
; XX
; DT   09-JUL-2001  (first entry)
; XX
; DE   Group II intron CCR5-435s exon binding site 1 region.
; XX
; KW   Group II intron; CCR5-435s; CCR5; chemokine receptor; human;
; KW   human immunodeficiency virus type 1; HIV-1; ss.
; XX
; OS   Synthetic.
; XX
; FH   Key             Location/Qualifiers
; FT   misc_binding    1
; FT                   /*tag= a
; FT                   /bound_moiety= "pBRR-CCR5(s)/Tet delta'"
; FT                   /standard_name= "delta"
; FT                   /note= "binds to base 34 of sequence in
; FT                         AAF30843"
; FT   misc_binding    3. .4
; FT                   /*tag= b
; FT                   /bound_moiety= "pBRR-CCR5(s)/Tet delta'"
; FT                   /standard_name= "delta"
; FT                   /note= "binds to bases 31-32 of sequence in
; FT                         AAF30843"
; FT   misc_binding    5. .7
; FT                   /*tag= c
; FT                   /bound_moiety= "pBRR-CCR5(s)/Tet IBS1"
; FT                   /standard_name= "exon binding site 1"
; FT                   /note= "binds to bases 28-30 of sequence in
; FT                         AAF30843"
; FT   misc_binding    9. .10
; FT                   /*tag= d
; FT                   /bound_moiety= "pBRR-CCR5(s)/Tet IBS1"
; FT                   /standard_name= "exon binding site 1"
; FT                   /note= "binds to bases 25-26 of sequence in
; FT                         AAF30843"
; XX
; PN   WO200129059-A1.
; XX
; PD   26-APR-2001.
; XX
; PF   13-OCT-2000; 2000WO-US28485.
; XX
; PR   15-OCT-1999;   99US-0159724.
; PR   13-OCT-2000; 2000US-0159724.
; XX
; PA   (OHIS ) UNIV OHIO STATE RES FOUND.
; XX
; PI   Lambowitz AM,  Guo H,  Karberg M;
; XX
; DR   WPI; 2001-316240/33.
; XX
; PT   Novel construct comprising a modified group II intron sequence
; PT   comprising modified EBS1, EBS2 or delta sequence, or partially deleted
; PT   loop sequence in domain IV, and promoter for regulating intron
; PT   transcription -
; XX
; PS   Example 3; Fig 4B; 61pp; English.
; XX
; CC   The present sequence is that of the exon binding site 1 (EBS1)
; CC   and delta region element of a group II intron sequence selected to
; CC   specifically base pair with a target region (see AAF30843) within
; CC   the human CCR5 chemokine receptor gene.  The target region was
; CC   identified in a screening of CCR5 DNA for sequences matching the
; CC   wild-type DNA target site (see AAF30827) of the L1.LtrB group II
; CC   intron (see AAF30828) of Lactococcus lactis.  The intron,
; CC   designated CCR5-435s (435s indicating the insertion site on the
; CC   sense strand of the CCR5 gene) and also including an EBS2 site
; CC   (5'GUGACG) was identified following cloning of the target sequence
; CC   into a recipient vector and selecting introns from a combinatorial
; CC   library having randomised target site recognition sequences (EBS
; CC   and delta).  The selected intron CCR5-435s demonstrated a targeting
; CC   frequency of 1.5% in Escherichia coli cells following IPTG
; CC   induction.  Other selected introns were demonstrated to function in
; CC   human cells.  This is an example of the selection of group II introns
; CC   that specifically integrate into specific DNA target sites.  In the
; CC   present case, inactivation of the CCR5 gene may provide a means of
; CC   blocking HIV-1 infection and AIDS progression.
; XX
; SQ   Sequence 11 BP; 3 A; 4 C; 2 G; 2 U; 0 other;
;
;  AAF30844  Length: 11  October 2, 2003 14:58  Type: N  Check: 4634  ..
aaf30844

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3320 TCAGGGGTT 3328
              |||||||||
Db         10 TCAGGGGTT 2


RESULT 19
abq87139
;  TOIG of: abq87139  check: 4715  from: 1  to: 11
;
; ID   ABQ87139 standard; cDNA; 11 BP.
; XX
; AC   ABQ87139;
; XX
; DT   10-SEP-2002  (first entry)
; XX
; DE   Human skin stress/ageing related EST SEQ ID NO 894.
; XX
; KW   Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
; XX
; OS   Homo sapiens.
; XX
```

```
; PN   WO200253773-A2.
; XX
; PD   11-JUL-2002.
; XX
; PF   20-DEC-2001; 2001WO-EP15178.
; XX
; PR   03-JAN-2001; 2001DE-1000121.
; XX
; PA   (HENK ) HENKEL KGAA.
; XX
; PI   Petersohn D,  Conradt M,  Hofmann K;
; XX
; DR   WPI; 2002-528865/56.
; XX
; PT   Identifying genes involved in skin stress and ageing, useful e.g. in
; PT   screening for cosmetic or therapeutic agents, based on differential
; PT   gene expression  -
; XX
; PS   Claim 8; Page 74; 325pp; German.
; XX
; CC   The invention relates to identifying (M1) genes in vitro that, in humans
; CC   or animals, are important for skin ageing and/or skin stress by serial
; CC   analysis of gene expression between mixtures of transcribed and
; CC   optionally translated, genetically encoded factors (A) obtained from
; CC   young and aged skin, to identify that genes that show strong differential
; CC   expression. (A) comprises protein or mRNAs or their fragments. (M1) is
; CC   useful for: identifying markers of skin ageing and/or stress; determining
; CC   skin ageing and/or stress; and identifying or determining the effects of
; CC   pharmaceutical or cosmetic agents for control of skin ageing. The present
; CC   sequence is one of a group of human skin ageing/stress related expressed
; CC   sequence tags (ABQ86246-ABQ87680) of the invention.
; XX
; SQ   Sequence 11 BP; 2 A; 2 C; 5 G; 2 T; 0 other;
;
;  ABQ87139  Length: 11  October 2, 2003 14:58  Type: N  Check: 4715  ..
abq87139

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3324 GGGTTCCAG 3332
              |||||||||
Db          3 GGGTTCCAG 11


RESULT 20
abv63615
;  TOIG of: abv63615  check: 4819  from: 1  to: 11
;
; ID   ABV63615 standard; cDNA; 11 BP.
; XX
; AC   ABV63615;
; XX
; DT   21-OCT-2002  (first entry)
; XX
; DE   Human skin EST 1401.
; XX
; KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
; KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
; KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   WO200253774-A2.
; XX
; PD   11-JUL-2002.
; XX
; PF   20-DEC-2001; 2001WO-EP15179.
; XX
; PR   03-JAN-2001; 2001DE-1000127.
; XX
; PA   (HENK ) HENKEL KGAA.
; XX
; PI   Petersohn D,  Conradt M,  Hofmann K;
; XX
; DR   WPI; 2002-590638/63.
; XX
; PT   In vitro identification of skin-expressed genes, useful for determining
; PT   homeostasis and identifying cosmetic or pharmaceutical agents against
; PT   e.g. skin cancer  -
; XX
; PS   Disclosure; Page 63; 1345pp; German.
; XX
; CC   The invention relates to in vitro identification (M1) of genes expressed
; CC   in the skin of humans or animals by subjecting a mixture of genetically
; CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
; CC   so as to identify skin-expressed genes and quantify their expression.
; CC   (M1) is useful for identifying genes involved in skin homeostasis; to
; CC   determine skin homeostasis and to test agent (A) that maintains or
; CC   promotes skin homeostasis or that can be used for treating skin
; CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
; CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
; CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
; CC   skin. The present sequence is that of a human expressed sequence tag
; CC   (EST) of the invention.
; XX
; SQ   Sequence 11 BP; 1 A; 3 C; 3 G; 4 T; 0 other;
;
;  ABV63615  Length: 11  October 2, 2003 14:58  Type: N  Check: 4819  ..
abv63615

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3325 GGTTCCAGC 3333
              |||||||||
Db          2 GGTTCCAGC 10


RESULT 21
abv64938
;  TOIG of: abv64938  check: 4678  from: 1  to: 11
;
; ID   ABV64938 standard; cDNA; 11 BP.
; XX
; AC   ABV64938;
; XX
; DT   21-OCT-2002  (first entry)
; XX
; DE   Human skin EST 2724.
; XX
; KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
; KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
; KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   WO200253774-A2.
; XX
; PD   11-JUL-2002.
; XX
; PF   20-DEC-2001; 2001WO-EP15179.
; XX
; PR   03-JAN-2001; 2001DE-1000127.
; XX
; PA   (HENK ) HENKEL KGAA.
; XX
; PI   Petersohn D,  Conradt M,  Hofmann K;
; XX
; DR   WPI; 2002-590638/63.
; XX
; PT   In vitro identification of skin-expressed genes, useful for determining
; PT   homeostasis and identifying cosmetic or pharmaceutical agents against
; PT   e.g. skin cancer  -
```

```
; XX
; PS   Disclosure; Page 100; 1345pp; German.
; XX
; CC   The invention relates to in vitro identification (M1) of genes expressed
; CC   in the skin of humans or animals by subjecting a mixture of genetically
; CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
; CC   so as to identify skin-expressed genes and quantify their expression.
; CC   (M1) is useful for identifying genes involved in skin homeostasis; to
; CC   determine skin homeostasis and to test agent (A) that maintains or
; CC   promotes skin homeostasis or that can be used for treating skin
; CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
; CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
; CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
; CC   skin. The present sequence is that of a human expressed sequence tag
; CC   (EST) of the invention.
; XX
; SQ   Sequence 11 BP; 2 A; 2 C; 4 G; 3 T; 0 other;
;
;  ABV64938  Length: 11  October 2, 2003 14:58  Type: N  Check: 4678  ..
abv64938

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3318 ATTCAGGGG 3326
              |||||||||
Db          2 ATTCAGGGG 10


RESULT 22
abv64961/c
;  TOIG of: abv64961  check: 4510  from: 1  to: 11
;
; ID   ABV64961 standard; cDNA; 11 BP.
; XX
; AC   ABV64961;
; XX
; DT   21-OCT-2002  (first entry)
; XX
; DE   Human skin EST 2747.
; XX
; KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
; KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
; KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   WO200253774-A2.
; XX
; PD   11-JUL-2002.
; XX
; PF   20-DEC-2001; 2001WO-EP15179.
; XX
; PR   03-JAN-2001; 2001DE-1000127.
; XX
; PA   (HENK ) HENKEL KGAA.
; XX
; PI   Petersohn D,  Conradt M,  Hofmann K;
; XX
; DR   WPI; 2002-590638/63.
; XX
; PT   In vitro identification of skin-expressed genes, useful for determining
; PT   homeostasis and identifying cosmetic or pharmaceutical agents against
; PT   e.g. skin cancer  -
; XX
; PS   Disclosure; Page 101; 1345pp; German.
; XX
; CC   The invention relates to in vitro identification (M1) of genes expressed
; CC   in the skin of humans or animals by subjecting a mixture of genetically
; CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
; CC   so as to identify skin-expressed genes and quantify their expression.
; CC   (M1) is useful for identifying genes involved in skin homeostasis; to
; CC   determine skin homeostasis and to test agent (A) that maintains or
; CC   promotes skin homeostasis or that can be used for treating skin
; CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
; CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
; CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
; CC   skin. The present sequence is that of a human expressed sequence tag
; CC   (EST) of the invention.
; XX
; SQ   Sequence 11 BP; 2 A; 4 C; 4 G; 1 T; 0 other;
;
;  ABV64961  Length: 11  October 2, 2003 14:58  Type: N  Check: 4510  ..
abv64961

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3323 GGGGTTCCA 3331
              |||||||||
Db         10 GGGGTTCCA 2


RESULT 23
abv65456
;  TOIG of: abv65456  check: 4715  from: 1  to: 11
;
; ID   ABV65456 standard; cDNA; 11 BP.
; XX
; AC   ABV65456;
; XX
; DT   21-OCT-2002  (first entry)
; XX
; DE   Human skin EST 3242.
; XX
; KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
; KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
; KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   WO200253774-A2.
; XX
; PD   11-JUL-2002.
; XX
; PF   20-DEC-2001; 2001WO-EP15179.
; XX
; PR   03-JAN-2001; 2001DE-1000127.
; XX
; PA   (HENK ) HENKEL KGAA.
; XX
; PI   Petersohn D,  Conradt M,  Hofmann K;
; XX
; DR   WPI; 2002-590638/63.
; XX
; PT   In vitro identification of skin-expressed genes, useful for determining
; PT   homeostasis and identifying cosmetic or pharmaceutical agents against
; PT   e.g. skin cancer  -
; XX
; PS   Disclosure; Page 115; 1345pp; German.
; XX
; CC   The invention relates to in vitro identification (M1) of genes expressed
; CC   in the skin of humans or animals by subjecting a mixture of genetically
; CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
; CC   so as to identify skin-expressed genes and quantify their expression.
; CC   (M1) is useful for identifying genes involved in skin homeostasis; to
; CC   determine skin homeostasis and to test agent (A) that maintains or
; CC   promotes skin homeostasis or that can be used for treating skin
; CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
; CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
; CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
; CC   skin. The present sequence is that of a human expressed sequence tag
; CC   (EST) of the invention.
; XX
```

```
; SQ   Sequence 11 BP; 2 A; 2 C; 5 G; 2 T; 0 other;
;
;  ABV65456  Length: 11  October 2, 2003 14:58  Type: N  Check: 4715  ..
abv65456

  Query Match            45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity  100.0%;  Pred. No. 22;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3324 GGGTTCCAG 3332
              |||||||||
Db          3 GGGTTCCAG 11


RESULT 24
abv71036
;  TOIG of: abv71036  check: 4819  from: 1  to: 11
;
; ID   ABV71036 standard; cDNA; 11 BP.
; XX
; AC   ABV71036;
; XX
; DT   21-OCT-2002  (first entry)
; XX
; DE   Human skin EST 8822.
; XX
; KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
; KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
; KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   WO200253774-A2.
; XX
; PD   11-JUL-2002.
; XX
; PF   20-DEC-2001; 2001WO-EP15179.
; XX
; PR   03-JAN-2001; 2001DE-1000127.
; XX
; PA   (HENK ) HENKEL KGAA.
; XX
; PI   Petersohn D,  Conradt M,  Hofmann K;
; XX
; DR   WPI; 2002-590638/63.
; XX
; PT   In vitro identification of skin-expressed genes, useful for determining
; PT   homeostasis and identifying cosmetic or pharmaceutical agents against
; PT   e.g. skin cancer  -
; XX
; PS   Claim 24; Page 283; 1345pp; German.
; XX
; CC   The invention relates to in vitro identification (M1) of genes expressed
; CC   in the skin of humans or animals by subjecting a mixture of genetically
; CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
; CC   so as to identify skin-expressed genes and quantify their expression.
; CC   (M1) is useful for identifying genes involved in skin homeostasis; to
; CC   determine skin homeostasis and to test agent (A) that maintains or
; CC   promotes skin homeostasis or that can be used for treating skin
; CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
; CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
; CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
; CC   skin. The present sequence is that of a human expressed sequence tag
; CC   (EST) of the invention.
; XX
; SQ   Sequence 11 BP; 1 A; 3 C; 3 G; 4 T; 0 other;
;
;  ABV71036  Length: 11  October 2, 2003 14:58  Type: N  Check: 4819  ..
abv71036

  Query Match            45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity  100.0%;  Pred. No. 22;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3325 GGTTCCAGC 3333
              |||||||||
Db          2 GGTTCCAGC 10


RESULT 25
aaa56134
;  TOIG of: aaa56134  check: 3920  from: 1  to: 10
;
; ID   AAA56134 standard; DNA; 10 BP.
; XX
; AC   AAA56134;
; XX
; DT   07-SEP-2000  (first entry)
; XX
; DE   Human monocyte gene Tag oligonucleotide sequence SEQ ID NO:28.
; XX
; KW   Human; monocyte; macrophage; GM-macrophage; M-macrophage; tag;
; KW   granulocyte-macrophage colony-stimulating factor; characterisation;
; KW   GM-CSF; identification; diagnosis; gene specificity; oncogenesis;
; KW   disease onset mechanism; genetic disease; drug development; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   WO200024892-A1.
; XX
; PD   04-MAY-2000.
; XX
; PF   28-OCT-1999;   99WO-JP05982.
; XX
; PR   28-OCT-1998;   98JP-0307532.
; XX
; PA   (NISC-) JAPAN SCI & TECHNOLOGY CORP.
; XX
; PI   Hashimoto S,  Matsushima K,  Suzuki T;
; XX
; DR   WPI; 2000-350734/30.
; XX
; PT   Genes most frequently expressed in human monocytes and GM-macrophages
; PT   and M-macrophages studied and with cDNAs characterized, for study of
; PT   gene specificity, disease onset mechanism, drug development and
; PT   diagnosis  -
; XX
; PS   Claim 1; Page 44; 138pp; Japanese.
; XX
; CC   The present invention describes 100 human genes, which are expressed
; CC   most frequently in human monocytes. The cDNA of each gene has a
; CC   sequence fully defined in the specification, and lacking the CATG
; CC   sequence located adjacent to polyA region. Also described are:
; CC   (1) an antibody specifically for the protein encoded by any of the
; CC   genes; (2) oligonucleotides obtained from the cDNA sequences;
; CC   (3) 380 human genes which are expressed most frequently in human
; CC   macrophages, differentiated from human monocytes by
; CC   granulocyte-macrophage colony-stimulating factor, the cDNA of each gene
; CC   has a fully defined sequence, given in the specification, lacking the
; CC   base sequence CATG located most closely to the poly A region;
; CC   (4) an antibody specifically for the protein encoded by any of the
; CC   genes of (3); and (5) oligonucleotides obtained from the cDNA sequences
; CC   of (3). The genes and cDNAs, are used for the study of gene specificity
; CC   and disease onset mechanism e.g. oncogenesis, genetic diseases, drug
; CC   development and diagnosis. AAA56107 to AAA56586 represent specifically
; CC   claimed oligonucleotide tag sequences for human genes expressed in
; CC   monocytes and macrophages.
; XX
; SQ   Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 other;
;
;  AAA56134  Length: 10  October 2, 2003 14:57  Type: N  Check: 3920  ..
aaa56134

  Query Match            42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity  90.0%;  Pred. No. 30;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy       3322 AGGGGTTCCA 3331
             |||| |||||
Db          1 AGGGCTTCCA 10


RESULT 26
aaa56289
;  TOIG of: aaa56289  check: 3920  from: 1  to: 10
;
; ID   AAA56289 standard; DNA; 10 BP.
; XX
; AC   AAA56289;
; XX
; DT   07-SEP-2000  (first entry)
; XX
; DE   Human macrophage gene Tag oligonucleotide sequence SEQ ID NO:183.
; XX
; KW   Human; monocyte; macrophage; GM-macrophage; M-macrophage; tag;
; KW   granulocyte-macrophage colony-stimulating factor; characterisation;
; KW   GM-CSF; identification; diagnosis; gene specificity; oncogenesis;
; KW   disease onset mechanism; genetic disease; drug development; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   WO200024892-A1.
; XX
; PD   04-MAY-2000.
; XX
; PF   28-OCT-1999;   99WO-JP05982.
; XX
; PR   28-OCT-1998;   98JP-0307532.
; XX
; PA   (NISC-) JAPAN SCI & TECHNOLOGY CORP.
; XX
; PI   Hashimoto S,  Matsushima K,  Suzuki T;
; XX
; DR   WPI; 2000-350734/30.
; XX
; PT   Genes most frequently expressed in human monocytes and GM-macrophages
; PT   and M-macrophages studied and with cDNAs characterized, for study of
; PT   gene specificity, disease onset mechanism, drug development and
; PT   diagnosis  -
; XX
; PS   Claim 7; Page 75; 138pp; Japanese.
; XX
; CC   The present invention describes 100 human genes, which are expressed
; CC   most frequently in human monocytes. The cDNA of each gene has a
; CC   sequence fully defined in the specification, and lacking the CATG
; CC   sequence located adjacent to polyA region. Also described are:
; CC   (1) an antibody specifically for the protein encoded by any of the
; CC   genes; (2) oligonucleotides obtained from the cDNA sequences;
; CC   (3) 380 human genes which are expressed most frequently in human
; CC   macrophages, differentiated from human monocytes by
; CC   granulocyte-macrophage colony-stimulating factor, the cDNA of each gene
; CC   has a fully defined sequence, given in the specification, lacking the
; CC   base sequence CATG located most closely to the poly A region;
; CC   (4) an antibody specifically for the protein encoded by any of the
; CC   genes of (3); and (5) oligonucleotides obtained from the cDNA sequences
; CC   of (3). The genes and cDNAs, are used for the study of gene specificity
; CC   and disease onset mechanism e.g. oncogenesis, genetic diseases, drug
; CC   development and diagnosis. AAA56107 to AAA56586 represent specifically
; CC   claimed oligonucleotide tag sequences for human genes expressed in
; CC   monocytes and macrophages.
; XX
; SQ   Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 other;
;
;  AAA56289  Length: 10  October 2, 2003 14:57  Type: N  Check: 3920  ..
aaa56289

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 30;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy       3322 AGGGGTTCCA 3331
             |||| |||||
Db          1 AGGGCTTCCA 10


RESULT 27
aaa56391
;  TOIG of: aaa56391  check: 3920  from: 1  to: 10
;
; ID   AAA56391 standard; DNA; 10 BP.
; XX
; AC   AAA56391;
; XX
; DT   07-SEP-2000  (first entry)
; XX
; DE   Human macrophage gene Tag oligonucleotide sequence SEQ ID NO:285.
; XX
; KW   Human; monocyte; macrophage; GM-macrophage; M-macrophage; tag;
; KW   granulocyte-macrophage colony-stimulating factor; characterisation;
; KW   GM-CSF; identification; diagnosis; gene specificity; oncogenesis;
; KW   disease onset mechanism; genetic disease; drug development; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   WO200024892-A1.
; XX
; PD   04-MAY-2000.
; XX
; PF   28-OCT-1999;   99WO-JP05982.
; XX
; PR   28-OCT-1998;   98JP-0307532.
; XX
; PA   (NISC-) JAPAN SCI & TECHNOLOGY CORP.
; XX
; PI   Hashimoto S,  Matsushima K,  Suzuki T;
; XX
; DR   WPI; 2000-350734/30.
; XX
; PT   Genes most frequently expressed in human monocytes and GM-macrophages
; PT   and M-macrophages studied and with cDNAs characterized, for study of
; PT   gene specificity, disease onset mechanism, drug development and
; PT   diagnosis  -
; XX
; PS   Claim 13; Page 96; 138pp; Japanese.
; XX
; CC   The present invention describes 100 human genes, which are expressed
; CC   most frequently in human monocytes. The cDNA of each gene has a
; CC   sequence fully defined in the specification, and lacking the CATG
; CC   sequence located adjacent to polyA region. Also described are:
; CC   (1) an antibody specifically for the protein encoded by any of the
; CC   genes; (2) oligonucleotides obtained from the cDNA sequences;
; CC   (3) 380 human genes which are expressed most frequently in human
; CC   macrophages, differentiated from human monocytes by
; CC   granulocyte-macrophage colony-stimulating factor, the cDNA of each gene
; CC   has a fully defined sequence, given in the specification, lacking the
; CC   base sequence CATG located most closely to the poly A region;
; CC   (4) an antibody specifically for the protein encoded by any of the
; CC   genes of (3); and (5) oligonucleotides obtained from the cDNA sequences
; CC   of (3). The genes and cDNAs, are used for the study of gene specificity
; CC   and disease onset mechanism e.g. oncogenesis, genetic diseases, drug
; CC   development and diagnosis. AAA56107 to AAA56586 represent specifically
; CC   claimed oligonucleotide tag sequences for human genes expressed in
; CC   monocytes and macrophages.
; XX
; SQ   Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 other;
;
;  AAA56391  Length: 10  October 2, 2003 14:57  Type: N  Check: 3920  ..
aaa56391

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 30;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy       3322 AGGGGTTCCA 3331
              |||| |||||
Db          1 AGGGCTTCCA 10


RESULT 28
aac73982
;  TOIG of: aac73982  check: 3920  from: 1  to: 10
;
; ID   AAC73982 standard; cDNA; 10 BP.
; XX
; AC   AAC73982;
; XX
; DT   02-FEB-2001  (first entry)
; XX
; DE   Human dendritic cell cDNA base sequence oligonucleotide #69.
; XX
; KW   Human; dendritic cell; monocyte; immune system; diagnosis; cancer;
; KW   autoimmune disease; tumour; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   WO200060074-A1.
; XX
; PD   12-OCT-2000.
; XX
; PF   30-MAR-2000; 2000WO-JP02019.
; XX
; PR   01-APR-1999;   99JP-0095481.
; XX
; PA   (NISC-) JAPAN SCI & TECHNOLOGY CORP.
; XX
; PI   Hashimoto S,  Matsushima K,  Suzuki T;
; XX
; DR   WPI; 2000-619172/59.
; XX
; PT   Groups of genes expressed in human dendritic cells at a greater or
; PT   lesser extent than in monocytes for investigation and diagnosis of
; PT   autoimmune disease and tumors -
; XX
; PS   Claim 1; Page 10; 95pp; Japanese.
; XX
; CC   The present invention describes a group of genes consisting of 100 genes
; CC   which are highly expressed in human dendritic cells; a group of genes
; CC   which are expressed at a higher frequency in human dendritic cells than
; CC   in human monocytes; and a group of genes which are expressed at lower
; CC   frequency in human dendritic cells than in human monocytes. Each group
; CC   of genes are characterised in that cDNAs of these genes respectively
; CC   have the base sequences of SEQ ID NO:1 to 100 (AAC73914 to AAC74013),
; CC   SEQ ID NO:101 to 200 (AAC74014 to AAC74113) and SEQ ID NO:201 to 300
; CC   (AAC74114 to AAC74213), each is continuous with the base sequence
; CC   5'-CATG-3' located most closely to the poly-A region. The sequences can
; CC   be used for the investigation of the role and mechanism of the
; CC   involvement of dendritic cells in the immune system and for the study and
; CC   diagnosis of diseases in which dendritic cells play a significant role,
; CC   e.g. cancers and autoimmune diseases.
; XX
; SQ   Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 other;
;
;  AAC73982  Length: 10  October 2, 2003 14:57  Type: N  Check: 3920  ..
aac73982

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 30;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3322 AGGGGTTCCA 3331
              |||| |||||
Db          1 AGGGCTTCCA 10


RESULT 29
aaf36987
;  TOIG of: aaf36987  check: 3940  from: 1  to: 10
;
; ID   AAF36987 standard; DNA; 10 BP.
; XX
; AC   AAF36987;
; XX
; DT   23-MAR-2001  (first entry)
; XX
; DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3726.
; XX
; KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
; KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
; KW   serial analysis of gene expression; antifungal; tag; identification;
; KW   linker; PCR primer; ds.
; XX
; OS   Saccharomyces cerevisiae.
; XX
; PN   WO200077214-A2.
; XX
; PD   21-DEC-2000.
; XX
; PF   14-JUN-2000; 2000WO-US16223.
; XX
; PR   16-JUN-1999;   99US-0335032.
; XX
; PA   (UYJO ) UNIV JOHNS HOPKINS.
; XX
; PI   Velculescu V,  Vogelstein B,  Kinzler K;
; XX
; DR   WPI; 2001-061874/07.
; XX
; PT   Yeast gene coding sequences comprising NORF genes with serial analysis
; PT   of gene expression (SAGE) tags, useful for studying, monitoring and
; PT   affecting phases of the cell cycle -
; XX
; PS   Example; Page 133; 419pp; English.
; XX
; CC   The present invention describes an isolated DNA molecule comprising a
; CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
; CC   previously assigned open reading frame; or nonannotated ORF) genes
; CC   comprising a SAGE (serial analysis of gene expression) tag. Also
; CC   described are: (1) a method (M1) of using NORF genes to affect the cell
; CC   cycle comprising administering a NORF gene whose expression varies by at
; CC   least 10% between any two phases of the cell cycle selected from log
; CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
; CC   antifungal drugs comprising: (a) contacting a test substance with a
; CC   yeast cell; and (b) monitoring expression of a NORF gene whose
; CC   expression varies as in M1, where a test substance which modifies the
; CC   expression of the yeast gene is a candidate antifungal drug; (3) a method
; CC   (M3) for identifying human genes which are involved in cell cycle
; CC   progression comprising contacting human DNA with a probe which comprises
; CC   at least 10 contiguous nucleotides of a NORF gene whose expression varies
; CC   as in M1; and (4) a method (M4) for identifying a candidate drug as a
; CC   member of a class of drugs having a characteristic effect on gene
; CC   expression in a yeast cell comprising contacting a yeast cell with a
; CC   candidate drug and monitoring expression in the yeast cell of at least 1
; CC   NORF gene whose expression is affected by the class of drugs. The NORF
; CC   genes may be used to study, monitor and affect phases of the cell cycle,
; CC   the differentially expressed genes may be used as markers of phases of
; CC   the cell cycle. The methods may be used to identify candidate drugs which
; CC   affect the cell cycle and for identification of antifungal drugs.
; CC   AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
; CC   the present invention. AAF33262 to AAF33267 represent linkers and PCR
; CC   primers used in the SAGE method, in the exemplification of the present
; CC   invention.
; XX
; SQ   Sequence 10 BP; 4 A; 1 C; 3 G; 2 T; 0 other;
;
;  AAF36987  Length: 10  October 2, 2003 14:57  Type: N  Check: 3940  ..
aaf36987

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
```

```
  Best Local Similarity   90.0%;  Pred. No. 30;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3314 AGGGATTCAG 3323
              | ||||||||
Db          1 AAGGATTCAG 10


RESULT 30
aaf39730
;  TOIG of: aaf39730  check: 3916  from: 1  to: 10
;
; ID   AAF39730 standard; DNA; 10 BP.
; XX
; AC   AAF39730;
; XX
; DT   23-MAR-2001  (first entry)
; XX
; DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6469.
; XX
; KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
; KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
; KW   serial analysis of gene expression; antifungal; tag; identification;
; KW   linker; PCR primer; ds.
; XX
; OS   Saccharomyces cerevisiae.
; XX
; PN   WO200077214-A2.
; XX
; PD   21-DEC-2000.
; XX
; PF   14-JUN-2000; 2000WO-US16223.
; XX
; PR   16-JUN-1999;   99US-0335032.
; XX
; PA   (UYJO ) UNIV JOHNS HOPKINS.
; XX
; PI   Velculescu V,  Vogelstein B,  Kinzler K;
; XX
; DR   WPI; 2001-061874/07.
; XX
; PT   Yeast gene coding sequences comprising NORF genes with serial analysis
; PT   of gene expression (SAGE) tags, useful for studying, monitoring and
; PT   affecting phases of the cell cycle -
; XX
; PS   Example; Page 231; 419pp; English.
; XX
; CC   The present invention describes an isolated DNA molecule comprising a
; CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
; CC   previously assigned open reading frame; or nonannotated ORF) genes
; CC   comprising a SAGE (serial analysis of gene expression) tag. Also
; CC   described are: (1) a method (M1) of using NORF genes to affect the cell
; CC   cycle comprising administering a NORF gene whose expression varies by at
; CC   least 10% between any two phases of the cell cycle selected from log
; CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
; CC   antifungal drugs comprising: (a) contacting a test substance with a
; CC   yeast cell; and (b) monitoring expression of a NORF gene whose
; CC   expression varies as in M1, where a test substance which modifies the
; CC   expression of the yeast gene is a candidate antifungal drug; (3) a method
; CC   (M3) for identifying human genes which are involved in cell cycle
; CC   progression comprising contacting human DNA with a probe which comprises
; CC   at least 10 contiguous nucleotides of a NORF gene whose expression varies
; CC   as in M1; and (4) a method (M4) for identifying a candidate drug as a
; CC   member of a class of drugs having a characteristic effect on gene
; CC   expression in a yeast cell comprising contacting a yeast cell with a
; CC   candidate drug and monitoring expression in the yeast cell of at least 1
; CC   NORF gene whose expression is affected by the class of drugs. The NORF
; CC   genes may be used to study, monitor and affect phases of the cell cycle,
; CC   the differentially expressed genes may be used as markers of phases of
; CC   the cell cycle. The methods may be used to identify candidate drugs which
; CC   affect the cell cycle and for identification of antifungal drugs.
; CC   AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
; CC   the present invention. AAF33262 to AAF33267 represent linkers and PCR
; CC   primers used in the SAGE method, in the exemplification of the present
; CC   invention.
; XX
; SQ   Sequence 10 BP; 3 A; 2 C; 3 G; 2 T; 0 other;
;
;  AAF39730  Length: 10  October 2, 2003 14:57  Type: N  Check: 3916  ..
aaf39730

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 30;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3322 AGGGGTTCCA 3331
              ||| ||||||
Db          1 AGGAGTTCCA 10


RESULT 31
aaf41037/c
;  TOIG of: aaf41037  check: 4002  from: 1  to: 10
;
; ID   AAF41037 standard; DNA; 10 BP.
; XX
; AC   AAF41037;
; XX
; DT   23-MAR-2001  (first entry)
; XX
; DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7776.
; XX
; KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
; KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
; KW   serial analysis of gene expression; antifungal; tag; identification;
; KW   linker; PCR primer; ds.
; XX
; OS   Saccharomyces cerevisiae.
; XX
; PN   WO200077214-A2.
; XX
; PD   21-DEC-2000.
; XX
; PF   14-JUN-2000; 2000WO-US16223.
; XX
; PR   16-JUN-1999;   99US-0335032.
; XX
; PA   (UYJO ) UNIV JOHNS HOPKINS.
; XX
; PI   Velculescu V,  Vogelstein B,  Kinzler K;
; XX
; DR   WPI; 2001-061874/07.
; XX
; PT   Yeast gene coding sequences comprising NORF genes with serial analysis
; PT   of gene expression (SAGE) tags, useful for studying, monitoring and
; PT   affecting phases of the cell cycle -
; XX
; PS   Example; Page 277; 419pp; English.
; XX
; CC   The present invention describes an isolated DNA molecule comprising a
; CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
; CC   previously assigned open reading frame; or nonannotated ORF) genes
; CC   comprising a SAGE (serial analysis of gene expression) tag. Also
; CC   described are: (1) a method (M1) of using NORF genes to affect the cell
; CC   cycle comprising administering a NORF gene whose expression varies by at
; CC   least 10% between any two phases of the cell cycle selected from log
; CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
; CC   antifungal drugs comprising: (a) contacting a test substance with a
; CC   yeast cell; and (b) monitoring expression of a NORF gene whose
; CC   expression varies as in M1, where a test substance which modifies the
; CC   expression of the yeast gene is a candidate antifungal drug; (3) a method
; CC   (M3) for identifying human genes which are involved in cell cycle
; CC   progression comprising contacting human DNA with a probe which comprises
; CC   at least 10 contiguous nucleotides of a NORF gene whose expression varies
; CC   as in M1; and (4) a method (M4) for identifying a candidate drug as a
; CC   member of a class of drugs having a characteristic effect on gene
```

```
; CC   expression in a yeast cell comprising contacting a yeast cell with a
; CC   candidate drug and monitoring expression in the yeast cell of at least 1
; CC   NORF gene whose expression is affected by the class of drugs. The NORF
; CC   genes may be used to study, monitor and affect phases of the cell cycle,
; CC   the differentially expressed genes may be used as markers of phases of
; CC   the cell cycle. The methods may be used to identify candidate drugs which
; CC   affect the cell cycle and for identification of antifungal drugs.
; CC   AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
; CC   the present invention. AAF33262 to AAF33267 represent linkers and PCR
; CC   primers used in the SAGE method, in the exemplification of the present
; CC   invention.
; XX
; SQ   Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 other;
;
;  AAF41037  Length: 10  October 2, 2003 14:57  Type: N  Check: 4002  ..
aaf41037

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 30;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3315 GGGATTCAGG 3324
              | ||||||||
Db         10 GAGATTCAGG 1


RESULT 32
aah19941/c
;  TOIG of: aah19941  check: 3925  from: 1  to: 10
;
; ID   AAH19941 standard; DNA; 10 BP.
; XX
; AC   AAH19941;
; XX
; DT   07-AUG-2001  (first entry)
; XX
; DE   Mouse Treg immunoregulatory network related tag #12.
; XX
; KW   Mouse; EST; expressed sequence tag; contig; immunoregulation;
; KW   immunosuppression; Treg immunoregulatory network; inflammatory;
; KW   immune disorder; T regulatory lymphocyte; T helper cell; dermatological;
; KW   antiinflammatory; immunosuppressive; antiarteriosclerotic; antiallergic;
; KW   antidiabetic; neuroprotective; osteopathic; antiarthritic; anti-ulcer;
; KW   rheumatoid arthritis; osteoarthritis; glomerular nephritis; diabetes;
; KW   inflammatory bowel disease; vascular disease; atherosclerosis; psoriasis;
; KW   vasculitis; skin disease; dermatitis; Crohn's disease; lung disease;
; KW   ulcerative colitis; lupus erythematosus; autoimmune disorder; emphysema;
; KW   hypersensitivity; multiple sclerosis; chronic bronchitis; asthma;
; KW   idiopathic pulmonary fibrosis; primer; probe; tag; ss.
; XX
; OS   Mus musculus.
; OS   Synthetic.
; XX
; PN   WO200127267-A2.
; XX
; PD   19-APR-2001.
; XX
; PF   06-OCT-2000; 2000WO-GB03821.
; XX
; PR   08-OCT-1999;   99GB-0023790.
; XX
; PA   (ISIS-) ISIS INNOVATION LTD.
; XX
; PI   Adams E,  Waldmann H,  Cobbold S,  Zelenika D;
; XX
; DR   WPI; 2001-300216/31.
; XX
; PT   Isolated genes differentially expressed in T helper 1 (Th1) and 2 (Th2)
; PT   and T regulatory (Treg) lymphocytes useful in prophylaxis, diagnosis
; PT   and therapy of inflammatory and immune diseases.  -
; XX
; PS   Example 4; Page 4; 29pp; English.
; XX
; CC   The present invention describes an isolated gene (I) obtainable by:
; CC   (a) comparing the expression of one or more genes in populations of T
; CC   helper 1 lymphocytes (Th1)-, Th2- and T regulatory cells (Treg)-enriched
; CC   cell populations to identify a gene which is differentially expressed in
; CC   the populations; and (b) isolating the gene. (I) can have dermatological,
; CC   antiinflammatory, immunosuppressive, antiarteriosclerotic, antiallergic,
; CC   antidiabetic, neuroprotective, osteopathic, antiarthritic and anti-ulcer
; CC   activities. (I) can be used in anti-inflammatory and immunoregulatory
; CC   compositions for use in therapy, prophylaxis, or diagnosis and/or in a
; CC   pharmaceutical excipient, a unit dosage form or in a form suitable for
; CC   local or systemic administration. Methods from the present invention can
; CC   be used for detecting Th1 and/or Th2 and/or Treg cells in a biological
; CC   sample, for cell typing or for determining the number of Th1 and/or Th2
; CC   and/or Treg cells in a biological sample. Diseases which may be treated
; CC   by compositions of the invention include rheumatoid and osteoarthritis,
; CC   glomerular nephritis, diabetes, inflammatory bowel disease, vascular
; CC   diseases e.g. atherosclerosis and vasculitis, skin diseases such as
; CC   psoriasis and dermatitis, Crohn's disease, ulcerative colitis, lupus
; CC   erythematosus, autoimmune disorders, hypersensitivity, multiple
; CC   sclerosis, and lung diseases e.g. chronic bronchitis, emphysema,
; CC   idiopathic pulmonary fibrosis and asthma. (I) can also be used as markers
; CC   for analysis of serum, urine and biopsy, particularly during and after
; CC   therapy for multiple sclerosis. AAH19930 to AAH20034 and AAB75133
; CC   represent sequence used in the exemplification of the present invention.
; XX
; SQ   Sequence 10 BP; 1 A; 5 C; 2 G; 2 T; 0 other;
;
;  AAH19941  Length: 10  October 2, 2003 14:57  Type: N  Check: 3925  ..
aah19941

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 30;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3316 GGATTCAGGG 3325
              ||| ||||||
Db         10 GGACTCAGGG 1


RESULT 33
aah32665
;  TOIG of: aah32665  check: 3920  from: 1  to: 10
;
; ID   AAH32665 standard; cDNA; 10 BP.
; XX
; AC   AAH32665;
; XX
; DT   13-AUG-2001  (first entry)
; XX
; DE   LPS activated human monocyte expression gene cDNA tag SEQ:38.
; XX
; KW   Human; LPS; lipopolysaccharide; monocyte expression gene; tag; EST;
; KW   expressed sequence tag; diagnosis; human disease; treatment; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   JP2001069993-A.
; XX
; PD   21-MAR-2001.
; XX
; PF   28-APR-2000; 2000JP-0131079.
; XX
; PR   08-JUL-1999;   99JP-0195103.
; XX
; PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
; XX
; DR   WPI; 2001-304369/32.
; XX
; PT   LPS activated human monocyte expression gene group  -
; XX
; PS   Claim 1; Page 17; 52pp; Japanese.
; XX
; CC   The present invention describes an lipopolysaccharide (LPS) activated
```

```
; CC   human monocyte expression gene group consisting of the high-ranking 50
; CC   genes of the highest expression among the genes expressed by human
; CC   monocyte stimulated by LPS in which the cDNA of each gene has the base
; CC   sequence of (AAH32628 to AAH32677) continuous to the base sequence
; CC   5'-CATG-3' nearest to the polyA region. The gene group is useful for the
; CC   development of new means for the diagnosis and the treatment of various
; CC   human diseases in which human monocyte plays an important role.
; CC   AAH32628 to AAH32943 represent specifically claimed LPS activated human
; CC   monocyte expression gene cDNA tags from the present invention. AAH32944
; CC   represents an LPS activated human monocyte expression gene cDNA sequence
; CC   encoding AAB98009, which are given in the exemplification of the present
; CC   invention.
; XX
; SQ   Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 other;
;
;  AAH32665  Length: 10  October 2, 2003 14:57  Type: N  Check: 3920  ..
aah32665

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 30;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3322 AGGGGTTCCA 3331
              |||| |||||
Db          1 AGGGCTTCCA 10


RESULT 34
aah32697/c
;  TOIG of: aah32697  check: 3919  from: 1  to: 10
;
; ID   AAH32697 standard; cDNA; 10 BP.
; XX
; AC   AAH32697;
; XX
; DT   13-AUG-2001  (first entry)
; XX
; DE   LPS activated human monocyte expression gene cDNA tag SEQ:70.
; XX
; KW   Human; LPS; lipopolysaccharide; monocyte expression gene; tag; EST;
; KW   expressed sequence tag; diagnosis; human disease; treatment; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   JP2001069993-A.
; XX
; PD   21-MAR-2001.
; XX
; PF   28-APR-2000; 2000JP-0131079.
; XX
; PR   08-JUL-1999;   99JP-0195103.
; XX
; PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
; XX
; DR   WPI; 2001-304369/32.
; XX
; PT   LPS activated human monocyte expression gene group  -
; XX
; PS   Claim 10; Page 20; 52pp; Japanese.
; XX
; CC   The present invention describes an lipopolysaccharide (LPS) activated
; CC   human monocyte expression gene group consisting of the high-ranking 50
; CC   genes of the highest expression among the genes expressed by human
; CC   monocyte stimulated by LPS in which the cDNA of each gene has the base
; CC   sequence of (AAH32628 to AAH32677) continuous to the base sequence
; CC   5'-CATG-3' nearest to the polyA region. The gene group is useful for the
; CC   development of new means for the diagnosis and the treatment of various
; CC   human diseases in which human monocyte plays an important role.
; CC   AAH32628 to AAH32943 represent specifically claimed LPS activated human
; CC   monocyte expression gene cDNA tags from the present invention. AAH32944
; CC   represents an LPS activated human monocyte expression gene cDNA sequence
; CC   encoding AAB98009, which are given in the exemplification of the present
; CC   invention.
; XX
; SQ   Sequence 10 BP; 1 A; 5 C; 2 G; 2 T; 0 other;
;
;  AAH32697  Length: 10  October 2, 2003 14:57  Type: N  Check: 3919  ..
aah32697

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 30;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3316 GGATTCAGGG 3325
              |||| |||||
Db         10 GGATCCAGGG 1


RESULT 35
aah63595
;  TOIG of: aah63595  check: 3920  from: 1  to: 10
;
; ID   AAH63595 standard; cDNA; 10 BP.
; XX
; AC   AAH63595;
; XX
; DT   20-SEP-2001  (first entry)
; XX
; DE   Human ubiquitously expressed transcriptome sequence SEQ ID NO: 435.
; XX
; KW   Human; transcriptome; gene expression pattern; cancer; drug screening;
; KW   cancer diagnosis; cell specific gene expression; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   WO200138577-A2.
; XX
; PD   31-MAY-2001.
; XX
; PF   21-NOV-2000; 2000WO-US31922.
; XX
; PR   24-NOV-1999;   99US-0448480.
; XX
; PA   (UYJO ) UNIV JOHNS HOPKINS.
; XX
; PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
; XX
; DR   WPI; 2001-367706/38.
; XX
; PT   New isolated polynucleotides, useful for identifying specific cell
; PT   type, such as cancer cell, comprises transcriptomes expressed in
; PT   particular cell types -
; XX
; PS   Claim 13; Page 48; 94pp; English.
; XX
; CC   The present invention describes a method of identifying the type of cell
; CC   in a sample, involving determining which of the sequences
; CC   AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
; CC   in the invention are cell-type specific, cancer specific or ubiquitously
; CC   expressed in humans. They can also be used to screen for drugs, reduce
; CC   cancer specific gene expression, standardise expression and restore the
; CC   function of a diseased cell or tissue. The present sequence is one of
; CC   the transcriptomes described in the exemplification of the invention.
; XX
; SQ   Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 other;
;
;  AAH63595  Length: 10  October 2, 2003 14:57  Type: N  Check: 3920  ..
aah63595

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 30;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3322 AGGGGTTCCA 3331
              |||| |||||
Db          1 AGGGCTTCCA 10
```

```
RESULT 36
aah64656
;  TOIG of: aah64656  check: 3920  from: 1  to: 10
;
; ID   AAH64656 standard; cDNA; 10 BP.
; XX
; AC   AAH64656;
; XX
; DT   20-SEP-2001  (first entry)
; XX
; DE   Human colon cancer associated transcriptome sequence SEQ ID NO: 1496.
; XX
; KW   Human; transcriptome; gene expression pattern; cancer; drug screening;
; KW   cancer diagnosis; cell specific gene expression; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   WO200138577-A2.
; XX
; PD   31-MAY-2001.
; XX
; PF   21-NOV-2000; 2000WO-US31922.
; XX
; PR   24-NOV-1999;   99US-0448480.
; XX
; PA   (UYJO ) UNIV JOHNS HOPKINS.
; XX
; PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
; XX
; DR   WPI; 2001-367706/38.
; XX
; PT   New isolated polynucleotides, useful for identifying specific cell
; PT   type, such as cancer cell, comprises transcriptomes expressed in
; PT   particular cell types -
; XX
; PS   Disclosure; Page 75; 94pp; English.
; XX
; CC   The present invention describes a method of identifying the type of cell
; CC   in a sample, involving determining which of the sequences
; CC   AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
; CC   in the invention are cell-type specific, cancer specific or ubiquitously
; CC   expressed in humans. They can also be used to screen for drugs, reduce
; CC   cancer specific gene expression, standardise expression and restore the
; CC   function of a diseased cell or tissue. The present sequence is one of
; CC   the transcriptomes described in the exemplification of the invention.
; XX
; SQ   Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 other;
;
;  AAH64656  Length: 10  October 2, 2003 14:57  Type: N  Check: 3920  ..
aah64656

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 30;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3322 AGGGGTTCCA 3331
              |||| |||||
Db          1 AGGGCTTCCA 10


RESULT 37
aah64706
;  TOIG of: aah64706  check: 3920  from: 1  to: 10
;
; ID   AAH64706 standard; cDNA; 10 BP.
; XX
; AC   AAH64706;
; XX
; DT   20-SEP-2001  (first entry)
; XX
; DE   Human highly expressed transcriptome sequence SEQ ID NO: 1544.
; XX
; KW   Human; transcriptome; gene expression pattern; cancer; drug screening;
; KW   cancer diagnosis; cell specific gene expression; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   WO200138577-A2.
; XX
; PD   31-MAY-2001.
; XX
; PF   21-NOV-2000; 2000WO-US31922.
; XX
; PR   24-NOV-1999;   99US-0448480.
; XX
; PA   (UYJO ) UNIV JOHNS HOPKINS.
; XX
; PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
; XX
; DR   WPI; 2001-367706/38.
; XX
; PT   New isolated polynucleotides, useful for identifying specific cell
; PT   type, such as cancer cell, comprises transcriptomes expressed in
; PT   particular cell types -
; XX
; PS   Disclosure; Page 76; 94pp; English.
; XX
; CC   The present invention describes a method of identifying the type of cell
; CC   in a sample, involving determining which of the sequences
; CC   AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
; CC   in the invention are cell-type specific, cancer specific or ubiquitously
; CC   expressed in humans. They can also be used to screen for drugs, reduce
; CC   cancer specific gene expression, standardise expression and restore the
; CC   function of a diseased cell or tissue. The present sequence is one of
; CC   the transcriptomes described in the exemplification of the invention.
; XX
; SQ   Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 other;
;
;  AAH64706  Length: 10  October 2, 2003 14:57  Type: N  Check: 3920  ..
aah64706

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 30;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3322 AGGGGTTCCA 3331
              |||| |||||
Db          1 AGGGCTTCCA 10


RESULT 38
aai67389/c
;  TOIG of: aai67389  check: 3735  from: 1  to: 10
;
; ID   AAI67389 standard; DNA; 10 BP.
; XX
; AC   AAI67389;
; XX
; DT   11-FEB-2002  (first entry)
; XX
; DE   Human FKBP8 gene polymorphism detecting primer.
; XX
; KW   FK506-binding protein 8; FKBP8; haplotyping; polymorphism; cancer;
; KW   immunosuppression; human; primer; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   WO200172965-A2.
; XX
; PD   04-OCT-2001.
; XX
; PF   26-MAR-2001; 2001WO-US09718.
; XX
; PR   24-MAR-2000; 2000US-192125P.
```

```
; XX
; PA   (GENA-) GENAISSANCE PHARM INC.
; XX
; PI   Anastasio AE,  Bentivegna SC,  Choi JY,  Kliem SE,  Koshy B;
; PI   Stephens JC;
; XX
; DR   WPI; 2001-626261/72.
; XX
; PT   New haplotypes of the FK506-binding protein 8 gene, useful for
; PT   genotyping that gene in individual and to design new therapy for
; PT   associated disease such as immunosuppression and cancer  -
; XX
; PS   Claim 16; Page 15; 98pp; English.
; XX
; CC   The invention relates to haplotyping the FK506-binding protein 8 (38kD)
; CC   (FKBP8) gene in an individual. The method involves determining the
; CC   identity of the nucleotide pair at one or more polymorphic sites selected
; CC   from P1 to P26 ( described in the specification). The invention is useful
; CC   to improve the efficiency and reliability of several steps in the
; CC   discovery and development of drugs for treating diseases associated with
; CC   FKBP8 activity, for example immunosuppression and cancer. Sequences
; CC   AAI67352-403 represent oligonucleotide primers for detecting FKBP8 gene
; CC   polymorphisms by primer extension techniques.
; XX
; SQ   Sequence 10 BP; 1 A; 6 C; 2 G; 1 T; 0 other;
;
;  AAI67389  Length: 10  October 2, 2003 14:57  Type: N  Check: 3735  ..
aai67389

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 30;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3323 GGGGTTCCAG 3332
              ||||| ||||
Db         10 GGGGTGCCAG 1


RESULT 39
aas19576/c
;  TOIG of: aas19576  check: 3804  from: 1  to: 10
;
; ID   AAS19576 standard; DNA; 10 BP.
; XX
; AC   AAS19576;
; XX
; DT   26-MAR-2002  (first entry)
; XX
; DE   Primer-extension oligonucleotide #7 to detect human MPL polymorphisms.
; XX
; KW   Human; single nucleotide polymorphism; SNP; MPL; chromosome 1p34;
; KW   myeloproliferative leukaemia virus oncogene; haplotyping; genotyping;
; KW   congenital amegakaryocytic thrombocytopaenia; CAMT; primer; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   WO200179232-A2.
; XX
; PD   25-OCT-2001.
; XX
; PF   16-APR-2001; 2001WO-US12301.
; XX
; PR   14-APR-2000; 2000US-197839P.
; XX
; PA   (GENA-) GENAISSANCE PHARM INC.
; XX
; PI   Chew A,  Choi JY,  Koshy B,  Stephens JC;
; XX
; DR   WPI; 2002-055251/07.
; XX
; PT   Nucleotide polymorphisms in the human myeloproliferative leukemia virus
; PT   oncogene (MPL) gene, useful for studying the function of and expressing
; PT   MPL protein for use in screening drugs for treating diseases related to
; PT   MPL activity -
; XX
; PS   Claim 17; Page 16; 85pp; English.
; XX
; CC   The present invention relates to novel single nucleotide polymorphisms
; CC   (SNPs) in the human myeloproliferative leukaemia virus oncogene (MPL)
; CC   gene located on chromosome 1p34, and methods for haplotyping and/or
; CC   genotyping the MPL gene. The methods of the invention make use of
; CC   allele-specific oligonucleotides (ASOs) as probes and primers and/or
; CC   primer-extension oligonucleotides for detecting MPL gene polymorphisms.
; CC   The polynucleotides and screened compounds are useful for the
; CC   treatment of diseases associated with MPL activity, such as
; CC   congenital amegakaryocytic thrombocytopaenia (CAMT).
; CC   AAS19570-AAS19607 represent primer-extension oligonucleotides for
; CC   detecting human MPL gene polymorphisms.
; XX
; SQ   Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 other;
;
;  AAS19576  Length: 10  October 2, 2003 14:58  Type: N  Check: 3804  ..
aas19576

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 30;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3319 TTCAGGGGTT 3328
              |||||||| |
Db         10 TTCAGGGGCT 1


RESULT 40
aas57315
;  TOIG of: aas57315  check: 3832  from: 1  to: 10
;
; ID   AAS57315 standard; DNA; 10 BP.
; XX
; AC   AAS57315;
; XX
; DT   16-JAN-2002  (first entry)
; XX
; DE   Human CHRNB2 allele specific oligonucleotide PCR primer terminus #40.
; XX
; KW   Human; cholinergic receptor, nicotinic, beta polypeptide 2; neuronal;
; KW   CHRNB2; memory disorder; Alzheimer's disease; epilepsy; learning;
; KW   chromosome 1q21; schizophrenia; attention deficit/hyperactivity disorder;
; KW   ADHD; autosomal dominant nocturnal frontal lobe epilepsy; ADNFLE; ss;
; KW   allele specific oligonucleotide; ASO; PCR primer.
; XX
; OS   Homo sapiens.
; XX
; PN   WO200174833-A2.
; XX
; PD   11-OCT-2001.
; XX
; PF   03-APR-2001; 2001WO-US10666.
; XX
; PR   03-APR-2000; 2000US-194155P.
; PR   13-JUL-2000; 2000US-217952P.
; XX
; PA   (GENA-) GENAISSANCE PHARM INC.
; XX
; PI   Choi JY,  Kliem SE,  Koshy B,  Lee HH,  Sanchis A;
; XX
; DR   WPI; 2001-626374/72.
; XX
; PT   Genotyping cholinergic receptor, nicotinic, beta-polypeptide 2 gene of
; PT   an individual involves determining for two copies of the gene, the
; PT   identity of nucleotide pair at polymorphic sites selected from PS1-24
; PT   -
; XX
; PS   Claim 17; Page 15; 82pp; English.
; XX
; CC   The invention relates to genotyping/haplotyping the cholinergic receptor,
```

```
; CC   nicotinic, beta-polypeptide 2 (neuronal) (CHRNB2) gene of an individual,
; CC   comprising determining for the two copies of the CHRNB2 gene present in
; CC   the individual, the identity of the nucleotide pair at one or more
; CC   polymorphic sites selected from PS1-24. Also include are oligonucleotides
; CC   for performing the method and the nucleotide sequence of the polymorphic
; CC   variants of CHRNB2. The method is useful for detecting novel CHRNB2
; CC   polymorphisms and for determining if an individual has a haplotype or
; CC   haplotype pairs defined in the specification and to validate CHRNB2 as a
; CC   candidate agent for treating a specific condition or disease predicted to
; CC   be associated with CHRNB2 activity (e.g. a memory disorder, Alzheimer's
; CC   disease, epilepsy, a learning disorder, schizophrenia, attention
; CC   deficit/hyperactivity disorder, (ADHD) and autosomal dominant nocturnal
; CC   frontal lobe epilepsy (ADNFLE)), and in the design of clinical trials
; CC   of candidate drugs for treating a specific condition or disease
; CC   predicted to be associated with CHRNB2 activity. The method is useful to
; CC   screen for compounds targeting CHRNB2 to treat a specific conditions or
; CC   disease associated with CHRNB2 activity. The polymorphic nucleic acids
; CC   are useful in studying the expression and function of CHRNB2, and in
; CC   expressing CHRNB2 protein for use in screening for candidate drugs to
; CC   treat diseases related to CHRNB2 activity and are useful for therapeutic
; CC   purposes. The CHRNB2 gene is located on chromosome 1q21. The present
; CC   sequence is an allele specific oligonucleotide (ASO) PCR primer (3'
; CC   terminus) for performing the method of the invention.
; XX
; SQ   Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 other;
;
;  AAS57315  Length: 10  October 2, 2003 14:57  Type: N  Check: 3832  ..
aas57315

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 30;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3323 GGGGTTCCAG 3332
              ||||| ||||
Db          1 GGGGTCCCAG 10


RESULT 41
aav35904/c
;  TOIG of: aav35904  check: 3860  from: 1  to: 10
;
; ID   AAV35904 standard; DNA; 10 BP.
; XX
; AC   AAV35904;
; XX
; DT   26-AUG-1998  (first entry)
; XX
; DE   Primer used in RAPD assay of the invention.
; XX
; KW   Rapid amplification of polymorphic DNA; RAPD; allele; breeding programme;
; KW   muscle fibre composition; Duroc pig; meat quality; PCR primer; ss.
; XX
; OS   Synthetic.
; OS   Sus sp.
; XX
; PN   WO9815837-A1.
; XX
; PD   16-APR-1998.
; XX
; PF   07-OCT-1997;   97WO-GB02741.
; XX
; PR   09-SEP-1997;   97GB-0019002.
; PR   07-OCT-1996;   96GB-0020904.
; PR   18-FEB-1997;   97GB-0003350.
; PR   20-MAR-1997;   97GB-0005796.
; XX
; PA   (MEAT-) MEAT & LIVESTOCK COMMISSION.
; XX
; PI   Maltin CA,  Steven J,  Warkup CC;
; XX
; DR   WPI; 1998-240968/21.
; XX
; PT   Assay for alleles or muscle fibre composition characteristic of
; PT   Duroc type pigs - comprises determination of genotype or muscle
; PT   fibre properties, used to identify animals for breeding programs and
; PT   to assess meat quality
; XX
; PS   Example 3; Page 32; 56pp; English.
; XX
; CC   PCR primers AAV35877-996 were used in a rapid amplification of
; CC   polymorphic DNA (RAPD) reaction in the assay of the invention. This assay
; CC   is used to determine if an animal has an allele for, or muscle fibre
; CC   composition (MFC) characteristic of, the Duroc pig. Duroc pigs produce
; CC   meat of superior quality (particularly tenderness) but are normally less
; CC   efficient feed converters and fatter than other types. The assay
; CC   comprises analysing a tissue sample to determine if the genotype
; CC   comprises the allele, and genetic features typical of animals with
; CC   Duroc-type MFC are present. The method is used to select animals that
; CC   have Duroc characteristics for use in breeding programmes (to develop
; CC   the animals with Duroc pig characteristics), and to assess meat quality.
; XX
; SQ   Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 other;
;
;  AAV35904  Length: 10  October 2, 2003 14:57  Type: N  Check: 3860  ..
aav35904

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 30;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3321 CAGGGGTTCC 3330
              || |||||||
Db          10 CATGGGTTCC 1


RESULT 42
aaz83394/c
;  TOIG of: aaz83394  check: 3837  from: 1  to: 10
;
; ID   AAZ83394 standard; DNA; 10 BP.
; XX
; AC   AAZ83394;
; XX
; DT   07-APR-2000  (first entry)
; XX
; DE   Metastatic breast tumour cell upregulated transcript tag #2628.
; XX
; KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
; KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
; KW   antimetastatic; vaccine; diagnosis; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   WO9965928-A2.
; XX
; PD   23-DEC-1999.
; XX
; PF   18-JUN-1999;   99WO-US13647.
; XX
; PR   19-JUN-1998;   98US-0089853.
; PR   19-JUN-1998;   98US-0089997.
; PR   19-JUN-1998;   98US-0090039.
; PR   19-JUN-1998;   98US-0090040.
; PR   19-JUN-1998;   98US-0090041.
; XX
; PA   (GENZ ) GENZYME CORP.
; PA   (ROBE/) ROBERTS B L.
; PA   (SHAN/) SHANKARA S.
; XX
; PI   Roberts BL,  Shankara S;
; XX
; DR   WPI; 2000-106079/09.
; XX
; PT   Isolated polynucleotides differentially expressed between metastatic
; PT   and non-metastatic breast cancer cells, useful for diagnosis,
```

```
; PT   prevention and treatment of cancer -
; XX
; PS   Claim 1; Page 129; 219pp; English.
; XX
; CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
; CC   transcripts that are preferentially transcribed in the metastatic breast
; CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
; CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
; CC   that are preferentially transcribed in the primary or non-metastatic
; CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
; CC   cells). These transcripts can be used for diagnosis, prognosis,
; CC   monitoring and treatment of breast cancer, particularly where metastatic.
; CC   Diagnosis is by standard immunoassays or hybridisation/amplification
; CC   reactions. Compounds that modulate expression of the transcripts are
; CC   potentially useful for treatment of (metastatic) breast cancer, while
; CC   promoters from the transcripts are used to direct expression, in selected
; CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
; CC   sequences), particularly an antigen-encoding sequence for use in gene or
; CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
; CC   useful in vaccines; for diagnosing breast cancer and for raising
; CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
; CC   therapeutic agents. Host cells that produce the polypeptides can be used
; CC   to expand and isolate populations of educated, antigen-specific immune
; CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
; CC   adoptive immunotherapy.
; XX
; SQ   Sequence 10 BP; 2 A; 5 C; 2 G; 1 T; 0 other;
;
;  AAZ83394  Length: 10  October 2, 2003 14:57  Type: N  Check: 3837  ..
aaz83394

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 30;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3320 TCAGGGGTTC 3329
              ||||||| ||
Db         10 TCAGGGGGTC 1


RESULT 43
aaz83550/c
;  TOIG of: aaz83550  check: 3859  from: 1  to: 10
;
; ID   AAZ83550 standard; DNA; 10 BP.
; XX
; AC   AAZ83550;
; XX
; DT   07-APR-2000  (first entry)
; XX
; DE   Metastatic breast tumour cell upregulated transcript tag #2784.
; XX
; KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
; KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
; KW   antimetastatic; vaccine; diagnosis; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   WO9965928-A2.
; XX
; PD   23-DEC-1999.
; XX
; PF   18-JUN-1999;   99WO-US13647.
; XX
; PR   19-JUN-1998;   98US-0089853.
; PR   19-JUN-1998;   98US-0089997.
; PR   19-JUN-1998;   98US-0090039.
; PR   19-JUN-1998;   98US-0090040.
; PR   19-JUN-1998;   98US-0090041.
; XX
; PA   (GENZ ) GENZYME CORP.
; PA   (ROBE/) ROBERTS B L.
; PA   (SHAN/) SHANKARA S.
; XX
; PI   Roberts BL,  Shankara S;
; XX
; DR   WPI; 2000-106079/09.
; XX
; PT   Isolated polynucleotides differentially expressed between metastatic
; PT   and non-metastatic breast cancer cells, useful for diagnosis,
; PT   prevention and treatment of cancer -
; XX
; PS   Claim 1; Page 133; 219pp; English.
; XX
; CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
; CC   transcripts that are preferentially transcribed in the metastatic breast
; CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
; CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
; CC   that are preferentially transcribed in the primary or non-metastatic
; CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
; CC   cells). These transcripts can be used for diagnosis, prognosis,
; CC   monitoring and treatment of breast cancer, particularly where metastatic.
; CC   Diagnosis is by standard immunoassays or hybridisation/amplification
; CC   reactions. Compounds that modulate expression of the transcripts are
; CC   potentially useful for treatment of (metastatic) breast cancer, while
; CC   promoters from the transcripts are used to direct expression, in selected
; CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
; CC   sequences), particularly an antigen-encoding sequence for use in gene or
; CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
; CC   useful in vaccines; for diagnosing breast cancer and for raising
; CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
; CC   therapeutic agents. Host cells that produce the polypeptides can be used
; CC   to expand and isolate populations of educated, antigen-specific immune
; CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
; CC   adoptive immunotherapy.
; XX
; SQ   Sequence 10 BP; 1 A; 6 C; 1 G; 2 T; 0 other;
;
;  AAZ83550  Length: 10  October 2, 2003 14:57  Type: N  Check: 3859  ..
aaz83550

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 30;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3315 GGGATTCAGG 3324
              ||||| ||||
Db         10 GGGATGCAGG 1


RESULT 44
aaz84309
;  TOIG of: aaz84309  check: 3871  from: 1  to: 10
;
; ID   AAZ84309 standard; DNA; 10 BP.
; XX
; AC   AAZ84309;
; XX
; DT   07-APR-2000  (first entry)
; XX
; DE   Metastatic breast tumour cell downregulated transcript tag #3543.
; XX
; KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
; KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
; KW   antimetastatic; vaccine; diagnosis; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   WO9965928-A2.
; XX
; PD   23-DEC-1999.
; XX
; PF   18-JUN-1999;   99WO-US13647.
; XX
; PR   19-JUN-1998;   98US-0089853.
; PR   19-JUN-1998;   98US-0089997.
```

```
; PR   19-JUN-1998;   98US-0090039.
; PR   19-JUN-1998;   98US-0090040.
; PR   19-JUN-1998;   98US-0090041.
; XX
; PA   (GENZ ) GENZYME CORP.
; PA   (ROBE/) ROBERTS B L.
; PA   (SHAN/) SHANKARA S.
; XX
; PI   Roberts BL,  Shankara S;
; XX
; DR   WPI; 2000-106079/09.
; XX
; PT   Isolated polynucleotides differentially expressed between metastatic
; PT   and non-metastatic breast cancer cells, useful for diagnosis,
; PT   prevention and treatment of cancer -
; XX
; PS   Claim 1; Page 153; 219pp; English.
; XX
; CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
; CC   transcripts that are preferentially transcribed in the metastatic breast
; CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
; CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
; CC   that are preferentially transcribed in the primary or non-metastatic
; CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
; CC   cells). These transcripts can be used for diagnosis, prognosis,
; CC   monitoring and treatment of breast cancer, particularly where metastatic.
; CC   Diagnosis is by standard immunoassays or hybridisation/amplification
; CC   reactions. Compounds that modulate expression of the transcripts are
; CC   potentially useful for treatment of (metastatic) breast cancer, while
; CC   promoters from the transcripts are used to direct expression, in selected
; CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
; CC   sequences), particularly an antigen-encoding sequence for use in gene or
; CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
; CC   useful in vaccines; for diagnosing breast cancer and for raising
; CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
; CC   therapeutic agents. Host cells that produce the polypeptides can be used
; CC   to expand and isolate populations of educated, antigen-specific immune
; CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
; CC   adoptive immunotherapy.
; XX
; SQ   Sequence 10 BP; 3 A; 1 C; 5 G; 1 T; 0 other;
;
;  AAZ84309  Length: 10  October 2, 2003 14:57  Type: N  Check: 3871  ..
aaz84309

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 30;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3317 GATTCAGGGG 3326
              || |||||||
Db          1 GAATCAGGGG 10


RESULT 45
aaz84773/c
;  TOIG of: aaz84773  check: 3863  from: 1  to: 10
;
; ID   AAZ84773 standard; DNA; 10 BP.
; XX
; AC   AAZ84773;
; XX
; DT   07-APR-2000  (first entry)
; XX
; DE   Metastatic breast tumour cell downregulated transcript tag #4007.
; XX
; KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
; KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
; KW   antimetastatic; vaccine; diagnosis; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   WO9965928-A2.
; XX
; PD   23-DEC-1999.
; XX
; PF   18-JUN-1999;   99WO-US13647.
; XX
; PR   19-JUN-1998;   98US-0089853.
; PR   19-JUN-1998;   98US-0089997.
; PR   19-JUN-1998;   98US-0090039.
; PR   19-JUN-1998;   98US-0090040.
; PR   19-JUN-1998;   98US-0090041.
; XX
; PA   (GENZ ) GENZYME CORP.
; PA   (ROBE/) ROBERTS B L.
; PA   (SHAN/) SHANKARA S.
; XX
; PI   Roberts BL,  Shankara S;
; XX
; DR   WPI; 2000-106079/09.
; XX
; PT   Isolated polynucleotides differentially expressed between metastatic
; PT   and non-metastatic breast cancer cells, useful for diagnosis,
; PT   prevention and treatment of cancer -
; XX
; PS   Claim 1; Page 165; 219pp; English.
; XX
; CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
; CC   transcripts that are preferentially transcribed in the metastatic breast
; CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
; CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
; CC   that are preferentially transcribed in the primary or non-metastatic
; CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
; CC   cells). These transcripts can be used for diagnosis, prognosis,
; CC   monitoring and treatment of breast cancer, particularly where metastatic.
; CC   Diagnosis is by standard immunoassays or hybridisation/amplification
; CC   reactions. Compounds that modulate expression of the transcripts are
; CC   potentially useful for treatment of (metastatic) breast cancer, while
; CC   promoters from the transcripts are used to direct expression, in selected
; CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
; CC   sequences), particularly an antigen-encoding sequence for use in gene or
; CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
; CC   useful in vaccines; for diagnosing breast cancer and for raising
; CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
; CC   therapeutic agents. Host cells that produce the polypeptides can be used
; CC   to expand and isolate populations of educated, antigen-specific immune
; CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
; CC   adoptive immunotherapy.
; XX
; SQ   Sequence 10 BP; 2 A; 6 C; 0 G; 2 T; 0 other;
;
;  AAZ84773  Length: 10  October 2, 2003 14:57  Type: N  Check: 3863  ..
aaz84773

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 30;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3316 GGATTCAGGG 3325
              ||||| ||||
Db         10 GGATTGAGGG 1


RESULT 46
aaz85387/c
;  TOIG of: aaz85387  check: 3959  from: 1  to: 10
;
; ID   AAZ85387 standard; DNA; 10 BP.
; XX
; AC   AAZ85387;
; XX
; DT   07-APR-2000  (first entry)
; XX
; DE   Metastatic breast tumour cell downregulated transcript tag #4621.
; XX
```

```
; KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
; KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
; KW   antimetastatic; vaccine; diagnosis; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   WO9965928-A2.
; XX
; PD   23-DEC-1999.
; XX
; PF   18-JUN-1999;   99WO-US13647.
; XX
; PR   19-JUN-1998;   98US-0089853.
; PR   19-JUN-1998;   98US-0089997.
; PR   19-JUN-1998;   98US-0090039.
; PR   19-JUN-1998;   98US-0090040.
; PR   19-JUN-1998;   98US-0090041.
; XX
; PA   (GENZ ) GENZYME CORP.
; PA   (ROBE/) ROBERTS B L.
; PA   (SHAN/) SHANKARA S.
; XX
; PI   Roberts BL,  Shankara S;
; XX
; DR   WPI; 2000-106079/09.
; XX
; PT   Isolated polynucleotides differentially expressed between metastatic
; PT   and non-metastatic breast cancer cells, useful for diagnosis,
; PT   prevention and treatment of cancer -
; XX
; PS   Claim 1; Page 183; 219pp; English.
; XX
; CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
; CC   transcripts that are preferentially transcribed in the metastatic breast
; CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
; CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
; CC   that are preferentially transcribed in the primary or non-metastatic
; CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
; CC   cells). These transcripts can be used for diagnosis, prognosis,
; CC   monitoring and treatment of breast cancer, particularly where metastatic.
; CC   Diagnosis is by standard immunoassays or hybridisation/amplification
; CC   reactions. Compounds that modulate expression of the transcripts are
; CC   potentially useful for treatment of (metastatic) breast cancer, while
; CC   promoters from the transcripts are used to direct expression, in selected
; CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
; CC   sequences), particularly an antigen-encoding sequence for use in gene or
; CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
; CC   useful in vaccines; for diagnosing breast cancer and for raising
; CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
; CC   therapeutic agents. Host cells that produce the polypeptides can be used
; CC   to expand and isolate populations of educated, antigen-specific immune
; CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
; CC   adoptive immunotherapy.
; XX
; SQ   Sequence 10 BP; 1 A; 5 C; 2 G; 2 T; 0 other;
;
;  AAZ85387  Length: 10  October 2, 2003 14:57  Type: N  Check: 3959  ..
aaz85387

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 30;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3317 GATTCAGGGG 3326
              ||| ||||||
Db         10 GATCCAGGGG 1


RESULT 47
aaz85591/c
;  TOIG of: aaz85591  check: 3944  from: 1  to: 10
;
; ID   AAZ85591 standard; DNA; 10 BP.
; XX
; AC   AAZ85591;
; XX
; DT   07-APR-2000  (first entry)
; XX
; DE   Metastatic breast tumour cell downregulated transcript tag #4825.
; XX
; KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
; KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
; KW   antimetastatic; vaccine; diagnosis; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   WO9965928-A2.
; XX
; PD   23-DEC-1999.
; XX
; PF   18-JUN-1999;   99WO-US13647.
; XX
; PR   19-JUN-1998;   98US-0089853.
; PR   19-JUN-1998;   98US-0089997.
; PR   19-JUN-1998;   98US-0090039.
; PR   19-JUN-1998;   98US-0090040.
; PR   19-JUN-1998;   98US-0090041.
; XX
; PA   (GENZ ) GENZYME CORP.
; PA   (ROBE/) ROBERTS B L.
; PA   (SHAN/) SHANKARA S.
; XX
; PI   Roberts BL,  Shankara S;
; XX
; DR   WPI; 2000-106079/09.
; XX
; PT   Isolated polynucleotides differentially expressed between metastatic
; PT   and non-metastatic breast cancer cells, useful for diagnosis,
; PT   prevention and treatment of cancer -
; XX
; PS   Claim 1; Page 188; 219pp; English.
; XX
; CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
; CC   transcripts that are preferentially transcribed in the metastatic breast
; CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
; CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
; CC   that are preferentially transcribed in the primary or non-metastatic
; CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
; CC   cells). These transcripts can be used for diagnosis, prognosis,
; CC   monitoring and treatment of breast cancer, particularly where metastatic.
; CC   Diagnosis is by standard immunoassays or hybridisation/amplification
; CC   reactions. Compounds that modulate expression of the transcripts are
; CC   potentially useful for treatment of (metastatic) breast cancer, while
; CC   promoters from the transcripts are used to direct expression, in selected
; CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
; CC   sequences), particularly an antigen-encoding sequence for use in gene or
; CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
; CC   useful in vaccines; for diagnosing breast cancer and for raising
; CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
; CC   therapeutic agents. Host cells that produce the polypeptides can be used
; CC   to expand and isolate populations of educated, antigen-specific immune
; CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
; CC   adoptive immunotherapy.
; XX
; SQ   Sequence 10 BP; 1 A; 5 C; 1 G; 3 T; 0 other;
;
;  AAZ85591  Length: 10  October 2, 2003 14:57  Type: N  Check: 3944  ..
aaz85591

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 30;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3315 GGGATTCAGG 3324
              ||||| ||||
Db         10 GGGATACAGG 1
```

```
RESULT 48
aaz85716/c
;  TOIG of: aaz85716  check: 3701  from: 1  to: 10
;
; ID   AAZ85716 standard; DNA; 10 BP.
; XX
; AC   AAZ85716;
; XX
; DT   07-APR-2000  (first entry)
; XX
; DE   Metastatic breast tumour cell downregulated transcript tag #4950.
; XX
; KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
; KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
; KW   antimetastatic; vaccine; diagnosis; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   WO9965928-A2.
; XX
; PD   23-DEC-1999.
; XX
; PF   18-JUN-1999;   99WO-US13647.
; XX
; PR   19-JUN-1998;   98US-0089853.
; PR   19-JUN-1998;   98US-0089997.
; PR   19-JUN-1998;   98US-0090039.
; PR   19-JUN-1998;   98US-0090040.
; PR   19-JUN-1998;   98US-0090041.
; XX
; PA   (GENZ ) GENZYME CORP.
; PA   (ROBE/) ROBERTS B L.
; PA   (SHAN/) SHANKARA S.
; XX
; PI   Roberts BL,  Shankara S;
; XX
; DR   WPI; 2000-106079/09.
; XX
; PT   Isolated polynucleotides differentially expressed between metastatic
; PT   and non-metastatic breast cancer cells, useful for diagnosis,
; PT   prevention and treatment of cancer -
; XX
; PS   Claim 1; Page 190; 219pp; English.
; XX
; CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
; CC   transcripts that are preferentially transcribed in the metastatic breast
; CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
; CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
; CC   that are preferentially transcribed in the primary or non-metastatic
; CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
; CC   cells). These transcripts can be used for diagnosis, prognosis,
; CC   monitoring and treatment of breast cancer, particularly where metastatic.
; CC   Diagnosis is by standard immunoassays or hybridisation/amplification
; CC   reactions. Compounds that modulate expression of the transcripts are
; CC   potentially useful for treatment of (metastatic) breast cancer, while
; CC   promoters from the transcripts are used to direct expression, in selected
; CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
; CC   sequences), particularly an antigen-encoding sequence for use in gene or
; CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
; CC   useful in vaccines; for diagnosing breast cancer and for raising
; CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
; CC   therapeutic agents. Host cells that produce the polypeptides can be used
; CC   to expand and isolate populations of educated, antigen-specific immune
; CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
; CC   adoptive immunotherapy.
; XX
; SQ   Sequence 10 BP; 3 A; 5 C; 1 G; 1 T; 0 other;
;
;  AAZ85716  Length: 10  October 2, 2003 14:57  Type: N  Check: 3701  ..
aaz85716

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 30;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3323 GGGGTTCCAG 3332
              |||||| |||
Db         10 GGGGTTTCAG 1


RESULT 49
aba06128
;  TOIG of: aba06128  check: 3920  from: 1  to: 10
;
; ID   ABA06128 standard; cDNA; 10 BP.
; XX
; AC   ABA06128;
; XX
; DT   10-JAN-2002  (first entry)
; XX
; DE   Human normal hepatocyte expression gene cDNA, SEQ ID NO: 105.
; XX
; KW   Human; hepatocyte; gene expression; hepatopathy; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   JP2001211883-A.
; XX
; PD   07-AUG-2001.
; XX
; PF   31-JAN-2000; 2000JP-0023170.
; XX
; PR   31-JAN-2000; 2000JP-0023170.
; XX
; PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
; XX
; DR   WPI; 2001-629566/73.
; XX
; PT   Human normal hepatocyte expression gene group  -
; XX
; PS   Claim 1; Page 8; 26pp; Japanese.
; XX
; CC   The invention relates to a human normal hepatocyte expression gene
; CC   group comprising 200 genes in the human normal hepatocyte. The
; CC   cDNA of each gene comprises one of 200 fully defined nucleotide
; CC   sequences as given in the specification. The gene group and the cDNAs
; CC   corresponding to each of the genes in the group are useful in the
; CC   diagnosis and treatment of human hepatopathy. The present sequence
; CC   is a cDNA corresponding to a gene expressed by normal human
; CC   hepatocytes.
; XX
; SQ   Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 other;
;
;  ABA06128  Length: 10  October 2, 2003 14:57  Type: N  Check: 3920  ..
aba06128

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 30;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3322 AGGGGTTCCA 3331
              |||| |||||
Db          1 AGGGCTTCCA 10


RESULT 50
abk23413
;  TOIG of: abk23413  check: 3920  from: 1  to: 10
;
; ID   ABK23413 standard; DNA; 10 BP.
; XX
; AC   ABK23413;
; XX
; DT   09-APR-2002  (first entry)
```

```
; XX
; DE   Transcript tag DNA sequence #2 induced or suppressed by N-myc.
; XX
; KW   Myc-dependent downstream gene; neoplastic; cancer; growth; invasion;
; KW   spread; myc target; myc tag; SAGE; serial analysis of gene expression;
; KW   myc oncogene; N-myc; human neuroblastoma; cytostatic; ds.
; XX
; OS   Homo sapiens.
; XX
; PN   WO200185941-A2.
; XX
; PD   15-NOV-2001.
; XX
; PF   11-MAY-2001; 2001WO-NL00361.
; XX
; PR   11-MAY-2000; 2000EP-0201698.
; PR   29-JUN-2000; 2000EP-0202284.
; XX
; PA   (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.
; XX
; PI   Versteeg R,  Caron HN;
; XX
; DR   WPI; 2002-066603/09.
; XX
; PT   A new nucleic acid library of myc-dependent downstream genes capable of
; PT   supporting a neoplastic characteristic of cancer is useful to find new
; PT   therapies and diagnoses for cancer  -
; XX
; PS   Disclosure; Page 49; 69pp; English.
; XX
; CC   The present invention relates to a nucleic acid library comprising
; CC   myc-dependent downstream genes or their functional fragments essentially
; CC   capable of supporting a neoplastic character of cancer such as growth,
; CC   invasion or spread. These myc target or tag sequences are identified
; CC   by SAGE (serial analysis of gene expression). The library is useful to
; CC   find new diagnoses and treatments for cancer. The invention is also
; CC   useful to enhance production of recombinant proteins in a production
; CC   system with high expression of endogenous or transfected myc oncogenes.
; CC   ABK23412-ABK23828 represent transcript tag DNA sequences that are
; CC   activated or repressed by N-myc in human neuroblastoma.
; XX
; SQ   Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 other;
;
;  ABK23413  Length: 10  October 2, 2003 14:57  Type: N  Check: 3920  ..
abk23413

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 30;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3322 AGGGGTTCCA 3331
              |||| |||||
Db          1 AGGGCTTCCA 10


RESULT 51
abk85685
;  TOIG of: abk85685  check: 3940  from: 1  to: 10
;
; ID   ABK85685 standard; DNA; 10 BP.
; XX
; AC   ABK85685;
; XX
; DT   15-AUG-2002  (first entry)
; XX
; DE   Human SCYB6 gene polymorphism detection oligonucleotide primer #6.
; XX
; KW   Human; small inducible cytokine subfamily B (Cys-X-Cys);
; KW   Member 6 (granulocyte chemotactic protein 2); SCYB6; primer; ss;
; KW   inflammatory disorder; cancer; antiinflammatory; cytostatic;
; KW   gene therapy; SCYB6 isogene expression modulator; SNP;
; KW   single nucleotide polymorphism.
; XX
; OS   Homo sapiens.
; XX
; PN   WO200227030-A1.
; XX
; PD   04-APR-2002.
; XX
; PF   27-SEP-2001; 2001WO-US30413.
; XX
; PR   27-SEP-2000; 2000US-235809P.
; XX
; PA   (GENA-) GENAISSANCE PHARM INC.
; XX
; PI   Anastasio AE,  Bentivegna SC,  Choi JY,  Monroe G,  Russo DP;
; XX
; DR   WPI; 2002-405057/43.
; XX
; PT   New isolated polymorphic variant of small inducible cytokine subfamily
; PT   B (Cys-X-Cys), Member 6 (granulocyte chemotactic protein 2) gene,
; PT   useful for expressing protein isoform used in drug screening techniques
; PT    -
; XX
; PS   Claim 16; Page 13; 71pp; English.
; XX
; CC   The present invention relates to a new polynucleotide having small
; CC   inducible cytokine subfamily B (Cys-X-Cys), Member 6 (granulocyte
; CC   chemotactic protein 2) (SCYB6) isogene. The invention is useful for
; CC   studying expression and function of SCYB6 and expressing SCYB6 protein
; CC   for use in screening for candidate drugs to treat diseases related to
; CC   SCYB6 activity. The polymorphism and haplotype data is useful for
; CC   validating whether SCYB6 is a suitable target for drugs to inflammatory
; CC   disorders and cancer, screening for such drugs and reducing bias
; CC   in clinical trials of such drugs. The invention is also useful for
; CC   therapeutic purposes. The method of the invention is useful for
; CC   identifying an association between susceptibility to a disease, staging
; CC   of a disease, or response to a drug. The present nucleic acid sequence
; CC   represents one of a collection of oligonucleotide primers (ABK85680-
; CC   ABK85697) that were used in the invention to detect polymorphisms in
; CC   the human SCYB6 gene.
; XX
; SQ   Sequence 10 BP; 3 A; 2 C; 3 G; 2 T; 0 other;
;
;  ABK85685  Length: 10  October 2, 2003 14:57  Type: N  Check: 3940  ..
abk85685

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 30;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3314 AGGGATTCAG 3323
              || |||||||
Db          1 AGCGATTCAG 10


RESULT 52
abl42689
;  TOIG of: abl42689  check: 3920  from: 1  to: 10
;
; ID   ABL42689 standard; cDNA; 10 BP.
; XX
; AC   ABL42689;
; XX
; DT   12-APR-2002  (first entry)
; XX
; DE   Human maturation/activation dendritic cell expression gene tag #63.
; XX
; KW   Human; maturation/activation dendritic cell expression gene; tag;
; KW   maturation; activation; dendritic cell; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   JP2001327293-A.
; XX
; PD   27-NOV-2001.
```

```
; XX
; PF   22-MAY-2000; 2000JP-0150562.
; XX
; PR   22-MAY-2000; 2000JP-0150562.
; XX
; PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
; XX
; DR   WPI; 2002-127070/17.
; XX
; PT   Human maturation/activation dendritic cell expression gene group -
; XX
; PS   Claim 1; Page 10; 41pp; Japanese.
; XX
; CC   The present invention describes a human maturation/activation dendritic
; CC   cell (DC) expression gene group consisting of 100 genes which show the
; CC   highest expression among the genes expressed in human maturation/
; CC   activation DC. Also described are: (1) a protein expressed by the above
; CC   human maturation/activation DC expression gene; (2) an antibody against
; CC   the protein; and (3) an antagonist against the expression of each gene
; CC   belonging to the above gene group. The gene group is useful for the
; CC   treatment and the diagnosis of various human diseases related to human
; CC   DC. ABL42627 to ABL42926 represent specifically claimed human
; CC   maturation/activation DC expression gene tags from the present invention.
; XX
; SQ   Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 other;
;
;  ABL42689  Length: 10  October 2, 2003 14:58  Type: N  Check: 3920  ..
abl42689

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 30;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3322 AGGGGTTCCA 3331
              |||| |||||
Db          1 AGGGCTTCCA 10


RESULT 53
abl42751/c
;  TOIG of: abl42751  check: 3846  from: 1  to: 10
;
; ID   ABL42751 standard; cDNA; 10 BP.
; XX
; AC   ABL42751;
; XX
; DT   12-APR-2002  (first entry)
; XX
; DE   Human maturation/activation dendritic cell expression gene tag #125.
; XX
; KW   Human; maturation/activation dendritic cell expression gene; tag;
; KW   maturation; activation; dendritic cell; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   JP2001327293-A.
; XX
; PD   27-NOV-2001.
; XX
; PF   22-MAY-2000; 2000JP-0150562.
; XX
; PR   22-MAY-2000; 2000JP-0150562.
; XX
; PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
; XX
; DR   WPI; 2002-127070/17.
; XX
; PT   Human maturation/activation dendritic cell expression gene group -
; XX
; PS   Claim 10; Page 12; 41pp; Japanese.
; XX
; CC   The present invention describes a human maturation/activation dendritic
; CC   cell (DC) expression gene group consisting of 100 genes which show the
; CC   highest expression among the genes expressed in human maturation/
; CC   activation DC. Also described are: (1) a protein expressed by the above
; CC   human maturation/activation DC expression gene; (2) an antibody against
; CC   the protein; and (3) an antagonist against the expression of each gene
; CC   belonging to the above gene group. The gene group is useful for the
; CC   treatment and the diagnosis of various human diseases related to human
; CC   DC. ABL42627 to ABL42926 represent specifically claimed human
; CC   maturation/activation DC expression gene tags from the present invention.
; XX
; SQ   Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 other;
;
;  ABL42751  Length: 10  October 2, 2003 14:58  Type: N  Check: 3846  ..
abl42751

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 30;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3319 TTCAGGGGTT 3328
              | ||||||||
Db         10 TCCAGGGGTT 1


RESULT 54
abl42815/c
;  TOIG of: abl42815  check: 3919  from: 1  to: 10
;
; ID   ABL42815 standard; cDNA; 10 BP.
; XX
; AC   ABL42815;
; XX
; DT   12-APR-2002  (first entry)
; XX
; DE   Human maturation/activation dendritic cell expression gene tag #189.
; XX
; KW   Human; maturation/activation dendritic cell expression gene; tag;
; KW   maturation; activation; dendritic cell; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   JP2001327293-A.
; XX
; PD   27-NOV-2001.
; XX
; PF   22-MAY-2000; 2000JP-0150562.
; XX
; PR   22-MAY-2000; 2000JP-0150562.
; XX
; PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
; XX
; DR   WPI; 2002-127070/17.
; XX
; PT   Human maturation/activation dendritic cell expression gene group -
; XX
; PS   Claim 10; Page 14; 41pp; Japanese.
; XX
; CC   The present invention describes a human maturation/activation dendritic
; CC   cell (DC) expression gene group consisting of 100 genes which show the
; CC   highest expression among the genes expressed in human maturation/
; CC   activation DC. Also described are: (1) a protein expressed by the above
; CC   human maturation/activation DC expression gene; (2) an antibody against
; CC   the protein; and (3) an antagonist against the expression of each gene
; CC   belonging to the above gene group. The gene group is useful for the
; CC   treatment and the diagnosis of various human diseases related to human
; CC   DC. ABL42627 to ABL42926 represent specifically claimed human
; CC   maturation/activation DC expression gene tags from the present invention.
; XX
; SQ   Sequence 10 BP; 1 A; 5 C; 2 G; 2 T; 0 other;
;
;  ABL42815  Length: 10  October 2, 2003 14:58  Type: N  Check: 3919  ..
abl42815

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
```

```
  Best Local Similarity   90.0%;  Pred. No. 30;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3316 GGATTCAGGG 3325
              |||| |||||
Db         10 GGATCCAGGG 1


RESULT 55
abq71536
;  TOIG of: abq71536  check: 3978  from: 1  to: 10
;
; ID   ABQ71536 standard; DNA; 10 BP.
; XX
; AC   ABQ71536;
; XX
; DT   28-AUG-2002  (first entry)
; XX
; DE   Zinc finger protein related oligonucleotide target SEQ ID NO:1270.
; XX
; KW   Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
; XX
; OS   Homo sapiens.
; OS   Synthetic.
; XX
; PN   WO200242459-A2.
; XX
; PD   30-MAY-2002.
; XX
; PF   20-NOV-2001; 2001WO-US43438.
; XX
; PR   20-NOV-2000; 2000US-0716637.
; XX
; PA   (SANG-) SANGAMO BIOSCIENCES INC.
; XX
; PI   Liu Q;
; XX
; DR   WPI; 2002-500284/53.
; XX
; PT   New zinc finger protein that binds to target site, useful in studying
; PT   gene function and for human therapeutics and plant engineering,
; PT   comprises first, second and third zinc fingers, ordered from N- to
; PT   C-terminus  -
; XX
; PS   Example 1; Page 47; 81pp; English.
; XX
; CC   The present invention describes a zinc finger protein (I) that binds to
; CC   a target site, comprising a first (F1), a second (F2), and a third (F3)
; CC   zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
; CC   target site comprises, in 3'-5' direction, a first (S1), a second (S2),
; CC   and a third (S3) target subsite. Also described are: (1) a polypeptide
; CC   (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
; CC   (3) designing (M) (I) involves selecting the F1 zinc finger such that
; CC   it binds to the S1 target subsite, selecting the F2 zinc finger such
; CC   that it binds to the S2 target subsite, and selecting the F3 zinc
; CC   finger such that it binds to the S3 target subsite, thus designing (I)
; CC   that binds to a target site. (I) is useful for recognition of triplet
; CC   target subsites having the nucleotide G in the 5'-most position of the
; CC   subsite. (I) is useful in studying gene function, and for human
; CC   therapeutics and plant engineering. (I), (II) or (III) is useful in
; CC   therapeutic methods to modulate the expression of a target region within
; CC   a subject, in diagnostic methods for sequence specific detection of
; CC   target nucleic acid in a sample, and in assays to determined the
; CC   phenotype and function of gene expression. (I) has improved affinity
; CC   and specificity for their target sequences, as well as enhanced
; CC   biological activity. ABQ71213 to ABQ72214 and ABP48191 to ABP51230
; CC   represent DNA target sequences and zinc finger peptides which are given
; CC   in the exemplification of the present invention.
; XX
; SQ   Sequence 10 BP; 3 A; 1 C; 3 G; 3 T; 0 other;
;
;  ABQ71536  Length: 10  October 2, 2003 14:57  Type: N  Check: 3978  ..
abq71536
```

```
  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 30;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3314 AGGGATTCAG 3323
              | ||||||||
Db          1 ATGGATTCAG 10


RESULT 56
abq71541
;  TOIG of: abq71541  check: 3978  from: 1  to: 10
;
; ID   ABQ71541 standard; DNA; 10 BP.
; XX
; AC   ABQ71541;
; XX
; DT   28-AUG-2002  (first entry)
; XX
; DE   Zinc finger protein related oligonucleotide target SEQ ID NO:1275.
; XX
; KW   Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
; XX
; OS   Homo sapiens.
; OS   Synthetic.
; XX
; PN   WO200242459-A2.
; XX
; PD   30-MAY-2002.
; XX
; PF   20-NOV-2001; 2001WO-US43438.
; XX
; PR   20-NOV-2000; 2000US-0716637.
; XX
; PA   (SANG-) SANGAMO BIOSCIENCES INC.
; XX
; PI   Liu Q;
; XX
; DR   WPI; 2002-500284/53.
; XX
; PT   New zinc finger protein that binds to target site, useful in studying
; PT   gene function and for human therapeutics and plant engineering,
; PT   comprises first, second and third zinc fingers, ordered from N- to
; PT   C-terminus  -
; XX
; PS   Example 1; Page 47; 81pp; English.
; XX
; CC   The present invention describes a zinc finger protein (I) that binds to
; CC   a target site, comprising a first (F1), a second (F2), and a third (F3)
; CC   zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
; CC   target site comprises, in 3'-5' direction, a first (S1), a second (S2),
; CC   and a third (S3) target subsite. Also described are: (1) a polypeptide
; CC   (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
; CC   (3) designing (M) (I) involves selecting the F1 zinc finger such that
; CC   it binds to the S1 target subsite, selecting the F2 zinc finger such
; CC   that it binds to the S2 target subsite, and selecting the F3 zinc
; CC   finger such that it binds to the S3 target subsite, thus designing (I)
; CC   that binds to a target site. (I) is useful for recognition of triplet
; CC   target subsites having the nucleotide G in the 5'-most position of the
; CC   subsite. (I) is useful in studying gene function, and for human
; CC   therapeutics and plant engineering. (I), (II) or (III) is useful in
; CC   therapeutic methods to modulate the expression of a target region within
; CC   a subject, in diagnostic methods for sequence specific detection of
; CC   target nucleic acid in a sample, and in assays to determined the
; CC   phenotype and function of gene expression. (I) has improved affinity
; CC   and specificity for their target sequences, as well as enhanced
; CC   biological activity. ABQ71213 to ABQ72214 and ABP48191 to ABP51230
; CC   represent DNA target sequences and zinc finger peptides which are given
; CC   in the exemplification of the present invention.
; XX
; SQ   Sequence 10 BP; 3 A; 1 C; 3 G; 3 T; 0 other;
;
```

```
;  ABQ71541  Length: 10  October 2, 2003 14:57  Type: N  Check: 3978  ..
abq71541

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 30;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3314 AGGGATTCAG 3323
              | ||||||||
Db          1 ATGGATTCAG 10


RESULT 57
abq71603
;  TOIG of: abq71603  check: 3978  from: 1  to: 10
;
; ID   ABQ71603 standard; DNA; 10 BP.
; XX
; AC   ABQ71603;
; XX
; DT   28-AUG-2002  (first entry)
; XX
; DE   Zinc finger protein related oligonucleotide target SEQ ID NO:1337.
; XX
; KW   Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
; XX
; OS   Homo sapiens.
; OS   Synthetic.
; XX
; PN   WO200242459-A2.
; XX
; PD   30-MAY-2002.
; XX
; PF   20-NOV-2001; 2001WO-US43438.
; XX
; PR   20-NOV-2000; 2000US-0716637.
; XX
; PA   (SANG-) SANGAMO BIOSCIENCES INC.
; XX
; PI   Liu Q;
; XX
; DR   WPI; 2002-500284/53.
; XX
; PT   New zinc finger protein that binds to target site, useful in studying
; PT   gene function and for human therapeutics and plant engineering,
; PT   comprises first, second and third zinc fingers, ordered from N- to
; PT   C-terminus  -
; XX
; PS   Example 1; Page 49; 81pp; English.
; XX
; CC   The present invention describes a zinc finger protein (I) that binds to
; CC   a target site, comprising a first (F1), a second (F2), and a third (F3)
; CC   zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
; CC   target site comprises, in 3'-5' direction, a first (S1), a second (S2),
; CC   and a third (S3) target subsite. Also described are: (1) a polypeptide
; CC   (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
; CC   (3) designing (M) (I) involves selecting the F1 zinc finger such that
; CC   it binds to the S1 target subsite, selecting the F2 zinc finger such
; CC   that it binds to the S2 target subsite, and selecting the F3 zinc
; CC   finger such that it binds to the S3 target subsite, thus designing (I)
; CC   that binds to a target site. (I) is useful for recognition of triplet
; CC   target subsites having the nucleotide G in the 5'-most position of the
; CC   subsite. (I) is useful in studying gene function, and for human
; CC   therapeutics and plant engineering. (I), (II) or (III) is useful in
; CC   therapeutic methods to modulate the expression of a target region within
; CC   a subject, in diagnostic methods for sequence specific detection of
; CC   target nucleic acid in a sample, and in assays to determined the
; CC   phenotype and function of gene expression. (I) has improved affinity
; CC   and specificity for their target sequences, as well as enhanced
; CC   biological activity. ABQ71213 to ABQ72214 and ABP48191 to ABP51230
; CC   represent DNA target sequences and zinc finger peptides which are given
; CC   in the exemplification of the present invention.
; XX
; SQ   Sequence 10 BP; 3 A; 1 C; 3 G; 3 T; 0 other;
;
;  ABQ71603  Length: 10  October 2, 2003 14:57  Type: N  Check: 3978  ..
abq71603

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 30;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3314 AGGGATTCAG 3323
              | ||||||||
Db          1 ATGGATTCAG 10


RESULT 58
aaa80926/c
;  TOIG of: aaa80926  check: 2610  from: 1  to: 8
;
; ID   AAA80926 standard; DNA; 8 BP.
; XX
; AC   AAA80926;
; XX
; DT   24-NOV-2000  (first entry)
; XX
; DE   A. thaliana primer walking octamer SEQ ID NO: 239.
; XX
; KW   Primer walking; octamer; primer; DNA sequencing; PCR; ss.
; XX
; OS   Arabidopsis thaliana.
; XX
; PN   US6083695-A.
; XX
; PD   04-JUL-2000.
; XX
; PF   21-MAY-1997;   97US-0859954.
; XX
; PR   15-APR-1996;   96US-0632782.
; XX
; PA   (UYHO-) UNIV HOUSTON.
; PA   (HARD/) HARDIN S H.
; XX
; PI   Hardin PE,  Hardin SH,  Homayouni R;
; XX
; DR   WPI; 2000-474852/41.
; XX
; PT   Sequencing an unknown DNA molecule for the polymerase chain reaction
; PT   and other primer processes comprises primer walking of octamer
; PT   oligonucleotides  -
; XX
; PS   Example 8; Column 145-146; 161pp; English.
; XX
; CC   This invention describes a novel method for sequencing an unknown DNA
; CC   molecule which comprises selecting a library primer from an octamer
; CC   oligonucleotide library consisting of 48 8-bp sequences and
; CC   corresponding complementary sequences, where the library primer is
; CC   complementary to a known sequence adjacent to the unknown sequence or
; CC   is complementary to a sequence in a known extension product. The method
; CC   is useful for DNA nucleotide sequencing, in PCR, and in other processes
; CC   which make use of primers.  The octamers are used to identify coding
; CC   sequences. Primer walking using the octamer libraries is advantageous
; CC   over other sequencing methods because it does not require multiple
; CC   cloning steps nor subsequent template preparations, and it is a
; CC   directed and methodical approach. AAA80688-A81253 represent the octamer
; CC   primers used in the primer walking method of the invention.
; XX
; SQ   Sequence 8 BP; 2 A; 3 C; 1 G; 2 T; 0 other;
;
;  AAA80926  Length: 8  October 2, 2003 14:57  Type: N  Check: 2610  ..
aaa80926

  Query Match             40.0%;  Score 8;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy       3314 AGGGATTC 3321
              ||||||||
Db          8 AGGGATTC 1


RESULT 59
aad45882
;  TOIG of: aad45882  check: 3937  from: 1  to: 10
;
; ID   AAD45882 standard; DNA; 10 BP.
; XX
; AC   AAD45882;
; XX
; DT   27-DEC-2002  (first entry)
; XX
; DE   Human TNF alpha gene polymorphism detecting primer #2.
; XX
; KW   Human; tumour necrosis factor; TNF alpha; cancer; inflammatory disorder;
; KW   diabetes; gene therapy; cytostatic; primer; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   WO200260918-A2.
; XX
; PD   08-AUG-2002.
; XX
; PF   03-DEC-2001; 2001WO-US46947.
; XX
; PR   01-DEC-2000; 2000US-250918P.
; XX
; PA   (GENA-) GENAISSANCE PHARM INC.
; XX
; PI   Bentivegna SC,  Denton RR,  Nandabalan K,  Sausker EA;
; XX
; DR   WPI; 2002-698545/75.
; XX
; PT   New genetic variants comprising human Tumor Necrosis Factor alpha (TNF)
; PT   isogene, useful for studying the expression and function of TNF and in
; PT   screening for drugs to treat cancer, diabetes or inflammatory disorders
; PT    -
; XX
; PS   Claim 17; Page 13; 66pp; English.
; XX
; CC   The present invention relates to novel genetic variants of human tumour
; CC   necrosis factor (TNF) alpha genes. The polymorphic variants are useful
; CC   in studying the expression and function of TNF, in expressing TNF protein
; CC   for use in screening for candidate drugs to treat diseases related to TNF
; CC   activity. The pharmaceutical compositions comprising TNF polynucleotide,
; CC   an antisense oligonucleotide directed against one of the novel TNF
; CC   isogenes, a polynucleotide encoding the antisense oligonucleotide or
; CC   another compound that inhibits expression of the TNF isogene are useful
; CC   for treating disorders affected by expression or function of the TNF
; CC   isogene e.g. cancer, diabetes or inflammatory disorders. Sequences of
; CC   the invention are also used in gene therapy. The present DNA sequence
; CC   is a primer used to detect human TNF alpha gene polymorphisms.
; XX
; SQ   Sequence 10 BP; 1 A; 1 C; 5 G; 3 T; 0 other;
;
;  AAD45882  Length: 10  October 2, 2003 14:58  Type: N  Check: 3937  ..
aad45882

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3319 TTCAGGGG 3326
              ||||||||
Db          2 TTCAGGGG 9


RESULT 60
aaf35691
```

```
;  TOIG of: aaf35691  check: 3887  from: 1  to: 10
;
; ID   AAF35691 standard; DNA; 10 BP.
; XX
; AC   AAF35691;
; XX
; DT   23-MAR-2001  (first entry)
; XX
; DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2430.
; XX
; KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
; KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
; KW   serial analysis of gene expression; antifungal; tag; identification;
; KW   linker; PCR primer; ds.
; XX
; OS   Saccharomyces cerevisiae.
; XX
; PN   WO200077214-A2.
; XX
; PD   21-DEC-2000.
; XX
; PF   14-JUN-2000; 2000WO-US16223.
; XX
; PR   16-JUN-1999;   99US-0335032.
; XX
; PA   (UYJO ) UNIV JOHNS HOPKINS.
; XX
; PI   Velculescu V,  Vogelstein B,  Kinzler K;
; XX
; DR   WPI; 2001-061874/07.
; XX
; PT   Yeast gene coding sequences comprising NORF genes with serial analysis
; PT   of gene expression (SAGE) tags, useful for studying, monitoring and
; PT   affecting phases of the cell cycle -
; XX
; PS   Example; Page 86; 419pp; English.
; XX
; CC   The present invention describes an isolated DNA molecule comprising a
; CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
; CC   previously assigned open reading frame; or nonannotated ORF) genes
; CC   comprising a SAGE (serial analysis of gene expression) tag. Also
; CC   described are: (1) a method (M1) of using NORF genes to affect the cell
; CC   cycle comprising administering a NORF gene whose expression varies by at
; CC   least 10% between any two phases of the cell cycle selected from log
; CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
; CC   antifungal drugs comprising: (a) contacting a test substance with a
; CC   yeast cell; and (b) monitoring expression of a NORF gene whose
; CC   expression varies as in M1, where a test substance which modifies the
; CC   expression of the yeast gene is a candidate antifungal drug; (3) a method
; CC   (M3) for identifying human genes which are involved in cell cycle
; CC   progression comprising contacting human DNA with a probe which comprises
; CC   at least 10 contiguous nucleotides of a NORF gene whose expression varies
; CC   as in M1; and (4) a method (M4) for identifying a candidate drug as a
; CC   member of a class of drugs having a characteristic effect on gene
; CC   expression in a yeast cell comprising contacting a yeast cell with a
; CC   candidate drug and monitoring expression in the yeast cell of at least 1
; CC   NORF gene whose expression is affected by the class of drugs. The NORF
; CC   genes may be used to study, monitor and affect phases of the cell cycle,
; CC   the differentially expressed genes may be used as markers of phases of
; CC   the cell cycle. The methods may be used to identify candidate drugs which
; CC   affect the cell cycle and for identification of antifungal drugs.
; CC   AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
; CC   the present invention. AAF33262 to AAF33267 represent linkers and PCR
; CC   primers used in the SAGE method, in the exemplification of the present
; CC   invention.
; XX
; SQ   Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 other;
;
;  AAF35691  Length: 10  October 2, 2003 14:58  Type: N  Check: 3887  ..
aaf35691

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 35;
```

```
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3324 GGGTTCCA 3331
              ||||||||
Db          2 GGGTTCCA 9


RESULT 61
aaf36466/c
;  TOIG of: aaf36466  check: 3858  from: 1  to: 10
;
; ID   AAF36466 standard; DNA; 10 BP.
; XX
; AC   AAF36466;
; XX
; DT   23-MAR-2001  (first entry)
; XX
; DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3205.
; XX
; KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
; KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
; KW   serial analysis of gene expression; antifungal; tag; identification;
; KW   linker; PCR primer; ds.
; XX
; OS   Saccharomyces cerevisiae.
; XX
; PN   WO200077214-A2.
; XX
; PD   21-DEC-2000.
; XX
; PF   14-JUN-2000; 2000WO-US16223.
; XX
; PR   16-JUN-1999;   99US-0335032.
; XX
; PA   (UYJO ) UNIV JOHNS HOPKINS.
; XX
; PI   Velculescu V,  Vogelstein B,  Kinzler K;
; XX
; DR   WPI; 2001-061874/07.
; XX
; PT   Yeast gene coding sequences comprising NORF genes with serial analysis
; PT   of gene expression (SAGE) tags, useful for studying, monitoring and
; PT   affecting phases of the cell cycle -
; XX
; PS   Example; Page 114; 419pp; English.
; XX
; CC   The present invention describes an isolated DNA molecule comprising a
; CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
; CC   previously assigned open reading frame; or nonannotated ORF) genes
; CC   comprising a SAGE (serial analysis of gene expression) tag. Also
; CC   described are: (1) a method (M1) of using NORF genes to affect the cell
; CC   cycle comprising administering a NORF gene whose expression varies by at
; CC   least 10% between any two phases of the cell cycle selected from log
; CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
; CC   antifungal drugs comprising: (a) contacting a test substance with a
; CC   yeast cell; and (b) monitoring expression of a NORF gene whose
; CC   expression varies as in M1, where a test substance which modifies the
; CC   expression of the yeast gene is a candidate antifungal drug; (3) a method
; CC   (M3) for identifying human genes which are involved in cell cycle
; CC   progression comprising contacting human DNA with a probe which comprises
; CC   at least 10 contiguous nucleotides of a NORF gene whose expression varies
; CC   as in M1; and (4) a method (M4) for identifying a candidate drug as a
; CC   member of a class of drugs having a characteristic effect on gene
; CC   expression in a yeast cell comprising contacting a yeast cell with a
; CC   candidate drug and monitoring expression in the yeast cell of at least 1
; CC   NORF gene whose expression is affected by the class of drugs. The NORF
; CC   genes may be used to study, monitor and affect phases of the cell cycle,
; CC   the differentially expressed genes may be used as markers of phases of
; CC   the cell cycle. The methods may be used to identify candidate drugs which
; CC   affect the cell cycle and for identification of antifungal drugs.
; CC   AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
; CC   the present invention. AAF33262 to AAF33267 represent linkers and PCR
; CC   primers used in the SAGE method, in the exemplification of the present
; CC   invention.
; XX
; SQ   Sequence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 other;
;
;  AAF36466  Length: 10  October 2, 2003 14:58  Type: N  Check: 3858  ..
aaf36466

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3325 GGTTCCAG 3332
              ||||||||
Db          8 GGTTCCAG 1


RESULT 62
aaf40055/c
;  TOIG of: aaf40055  check: 3949  from: 1  to: 10
;
; ID   AAF40055 standard; DNA; 10 BP.
; XX
; AC   AAF40055;
; XX
; DT   23-MAR-2001  (first entry)
; XX
; DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6794.
; XX
; KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
; KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
; KW   serial analysis of gene expression; antifungal; tag; identification;
; KW   linker; PCR primer; ds.
; XX
; OS   Saccharomyces cerevisiae.
; XX
; PN   WO200077214-A2.
; XX
; PD   21-DEC-2000.
; XX
; PF   14-JUN-2000; 2000WO-US16223.
; XX
; PR   16-JUN-1999;   99US-0335032.
; XX
; PA   (UYJO ) UNIV JOHNS HOPKINS.
; XX
; PI   Velculescu V,  Vogelstein B,  Kinzler K;
; XX
; DR   WPI; 2001-061874/07.
; XX
; PT   Yeast gene coding sequences comprising NORF genes with serial analysis
; PT   of gene expression (SAGE) tags, useful for studying, monitoring and
; PT   affecting phases of the cell cycle -
; XX
; PS   Example; Page 242; 419pp; English.
; XX
; CC   The present invention describes an isolated DNA molecule comprising a
; CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
; CC   previously assigned open reading frame; or nonannotated ORF) genes
; CC   comprising a SAGE (serial analysis of gene expression) tag. Also
; CC   described are: (1) a method (M1) of using NORF genes to affect the cell
; CC   cycle comprising administering a NORF gene whose expression varies by at
; CC   least 10% between any two phases of the cell cycle selected from log
; CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
; CC   antifungal drugs comprising: (a) contacting a test substance with a
; CC   yeast cell; and (b) monitoring expression of a NORF gene whose
; CC   expression varies as in M1, where a test substance which modifies the
; CC   expression of the yeast gene is a candidate antifungal drug; (3) a method
; CC   (M3) for identifying human genes which are involved in cell cycle
; CC   progression comprising contacting human DNA with a probe which comprises
; CC   at least 10 contiguous nucleotides of a NORF gene whose expression varies
; CC   as in M1; and (4) a method (M4) for identifying a candidate drug as a
; CC   member of a class of drugs having a characteristic effect on gene
; CC   expression in a yeast cell comprising contacting a yeast cell with a
```

```
; CC   candidate drug and monitoring expression in the yeast cell of at least 1
; CC   NORF gene whose expression is affected by the class of drugs. The NORF
; CC   genes may be used to study, monitor and affect phases of the cell cycle,
; CC   the differentially expressed genes may be used as markers of phases of
; CC   the cell cycle. The methods may be used to identify candidate drugs which
; CC   affect the cell cycle and for identification of antifungal drugs.
; CC   AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
; CC   the present invention. AAF33262 to AAF33267 represent linkers and PCR
; CC   primers used in the SAGE method, in the exemplification of the present
; CC   invention.
; XX
; SQ   Sequence 10 BP; 3 A; 3 C; 1 G; 3 T; 0 other;
;
;  AAF40055  Length: 10  October 2, 2003 14:58  Type: N  Check: 3949  ..
aaf40055

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3317 GATTCAGG 3324
              ||||||||
Db         10 GATTCAGG 3


RESULT 63
aaf42054
;  TOIG of: aaf42054  check: 4016  from: 1  to: 10
;
; ID   AAF42054 standard; DNA; 10 BP.
; XX
; AC   AAF42054;
; XX
; DT   23-MAR-2001  (first entry)
; XX
; DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8793.
; XX
; KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
; KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
; KW   serial analysis of gene expression; antifungal; tag; identification;
; KW   linker; PCR primer; ds.
; XX
; OS   Saccharomyces cerevisiae.
; XX
; PN   WO200077214-A2.
; XX
; PD   21-DEC-2000.
; XX
; PF   14-JUN-2000; 2000WO-US16223.
; XX
; PR   16-JUN-1999;   99US-0335032.
; XX
; PA   (UYJO ) UNIV JOHNS HOPKINS.
; XX
; PI   Velculescu V,  Vogelstein B,  Kinzler K;
; XX
; DR   WPI; 2001-061874/07.
; XX
; PT   Yeast gene coding sequences comprising NORF genes with serial analysis
; PT   of gene expression (SAGE) tags, useful for studying, monitoring and
; PT   affecting phases of the cell cycle -
; XX
; PS   Example; Page 314; 419pp; English.
; XX
; CC   The present invention describes an isolated DNA molecule comprising a
; CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
; CC   previously assigned open reading frame; or nonannotated ORF) genes
; CC   comprising a SAGE (serial analysis of gene expression) tag. Also
; CC   described are: (1) a method (M1) of using NORF genes to affect the cell
; CC   cycle comprising administering a NORF gene whose expression varies by at
; CC   least 10% between any two phases of the cell cycle selected from log
; CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
; CC   antifungal drugs comprising: (a) contacting a test substance with a
; CC   yeast cell; and (b) monitoring expression of a NORF gene whose
; CC   expression varies as in M1, where a test substance which modifies the
; CC   expression of the yeast gene is a candidate antifungal drug; (3) a method
; CC   (M3) for identifying human genes which are involved in cell cycle
; CC   progression comprising contacting human DNA with a probe which comprises
; CC   at least 10 contiguous nucleotides of a NORF gene whose expression varies
; CC   as in M1; and (4) a method (M4) for identifying a candidate drug as a
; CC   member of a class of drugs having a characteristic effect on gene
; CC   expression in a yeast cell comprising contacting a yeast cell with a
; CC   candidate drug and monitoring expression in the yeast cell of at least 1
; CC   NORF gene whose expression is affected by the class of drugs. The NORF
; CC   genes may be used to study, monitor and affect phases of the cell cycle,
; CC   the differentially expressed genes may be used as markers of phases of
; CC   the cell cycle. The methods may be used to identify candidate drugs which
; CC   affect the cell cycle and for identification of antifungal drugs.
; CC   AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
; CC   the present invention. AAF33262 to AAF33267 represent linkers and PCR
; CC   primers used in the SAGE method, in the exemplification of the present
; CC   invention.
; XX
; SQ   Sequence 10 BP; 2 A; 1 C; 5 G; 2 T; 0 other;
;
;  AAF42054  Length: 10  October 2, 2003 14:58  Type: N  Check: 4016  ..
aaf42054

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3314 AGGGATTC 3321
              ||||||||
Db          2 AGGGATTC 9


RESULT 64
aaf42057
;  TOIG of: aaf42057  check: 4052  from: 1  to: 10
;
; ID   AAF42057 standard; DNA; 10 BP.
; XX
; AC   AAF42057;
; XX
; DT   23-MAR-2001  (first entry)
; XX
; DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8796.
; XX
; KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
; KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
; KW   serial analysis of gene expression; antifungal; tag; identification;
; KW   linker; PCR primer; ds.
; XX
; OS   Saccharomyces cerevisiae.
; XX
; PN   WO200077214-A2.
; XX
; PD   21-DEC-2000.
; XX
; PF   14-JUN-2000; 2000WO-US16223.
; XX
; PR   16-JUN-1999;   99US-0335032.
; XX
; PA   (UYJO ) UNIV JOHNS HOPKINS.
; XX
; PI   Velculescu V,  Vogelstein B,  Kinzler K;
; XX
; DR   WPI; 2001-061874/07.
; XX
; PT   Yeast gene coding sequences comprising NORF genes with serial analysis
; PT   of gene expression (SAGE) tags, useful for studying, monitoring and
; PT   affecting phases of the cell cycle -
; XX
; PS   Example; Page 314; 419pp; English.
; XX
```

```
; CC   The present invention describes an isolated DNA molecule comprising a
; CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
; CC   previously assigned open reading frame; or nonannotated ORF) genes
; CC   comprising a SAGE (serial analysis of gene expression) tag. Also
; CC   described are: (1) a method (M1) of using NORF genes to affect the cell
; CC   cycle comprising administering a NORF gene whose expression varies by at
; CC   least 10% between any two phases of the cell cycle selected from log
; CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
; CC   antifungal drugs comprising: (a) contacting a test substance with a
; CC   yeast cell; and (b) monitoring expression of a NORF gene whose
; CC   expression varies as in M1, where a test substance which modifies the
; CC   expression of the yeast gene is a candidate antifungal drug; (3) a method
; CC   (M3) for identifying human genes which are involved in cell cycle
; CC   progression comprising contacting human DNA with a probe which comprises
; CC   at least 10 contiguous nucleotides of a NORF gene whose expression varies
; CC   as in M1; and (4) a method (M4) for identifying a candidate drug as a
; CC   member of a class of drugs having a characteristic effect on gene
; CC   expression in a yeast cell comprising contacting a yeast cell with a
; CC   candidate drug and monitoring expression in the yeast cell of at least 1
; CC   NORF gene whose expression is affected by the class of drugs. The NORF
; CC   genes may be used to study, monitor and affect phases of the cell cycle,
; CC   the differentially expressed genes may be used as markers of phases of
; CC   the cell cycle. The methods may be used to identify candidate drugs which
; CC   affect the cell cycle and for identification of antifungal drugs.
; CC   AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
; CC   the present invention. AAF33262 to AAF33267 represent linkers and PCR
; CC   primers used in the SAGE method, in the exemplification of the present
; CC   invention.
; XX
; SQ   Sequence 10 BP; 1 A; 1 C; 6 G; 2 T; 0 other;
;
;  AAF42057  Length: 10  October 2, 2003 14:58  Type: N  Check: 4052  ..
aaf42057

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3322 AGGGGTTC 3329
              ||||||||
Db          2 AGGGGTTC 9


RESULT 65
aaf42631
;  TOIG of: aaf42631  check: 4071  from: 1  to: 10
;
; ID   AAF42631 standard; DNA; 10 BP.
; XX
; AC   AAF42631;
; XX
; DT   23-MAR-2001  (first entry)
; XX
; DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:10770.
; XX
; KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
; KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
; KW   serial analysis of gene expression; antifungal; tag; identification;
; KW   linker; PCR primer; ds.
; XX
; OS   Saccharomyces cerevisiae.
; XX
; PN   WO200077214-A2.
; XX
; PD   21-DEC-2000.
; XX
; PF   14-JUN-2000; 2000WO-US16223.
; XX
; PR   16-JUN-1999;   99US-0335032.
; XX
; PA   (UYJO ) UNIV JOHNS HOPKINS.
; XX
; PI   Velculescu V,  Vogelstein B,  Kinzler K;
; XX
; DR   WPI; 2001-061874/07.
; XX
; PT   Yeast gene coding sequences comprising NORF genes with serial analysis
; PT   of gene expression (SAGE) tags, useful for studying, monitoring and
; PT   affecting phases of the cell cycle -
; XX
; PS   Example; Page 334; 419pp; English.
; XX
; CC   The present invention describes an isolated DNA molecule comprising a
; CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
; CC   previously assigned open reading frame; or nonannotated ORF) genes
; CC   comprising a SAGE (serial analysis of gene expression) tag. Also
; CC   described are: (1) a method (M1) of using NORF genes to affect the cell
; CC   cycle comprising administering a NORF gene whose expression varies by at
; CC   least 10% between any two phases of the cell cycle selected from log
; CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
; CC   antifungal drugs comprising: (a) contacting a test substance with a
; CC   yeast cell; and (b) monitoring expression of a NORF gene whose
; CC   expression varies as in M1, where a test substance which modifies the
; CC   expression of the yeast gene is a candidate antifungal drug; (3) a method
; CC   (M3) for identifying human genes which are involved in cell cycle
; CC   progression comprising contacting human DNA with a probe which comprises
; CC   at least 10 contiguous nucleotides of a NORF gene whose expression varies
; CC   as in M1; and (4) a method (M4) for identifying a candidate drug as a
; CC   member of a class of drugs having a characteristic effect on gene
; CC   expression in a yeast cell comprising contacting a yeast cell with a
; CC   candidate drug and monitoring expression in the yeast cell of at least 1
; CC   NORF gene whose expression is affected by the class of drugs. The NORF
; CC   genes may be used to study, monitor and affect phases of the cell cycle,
; CC   the differentially expressed genes may be used as markers of phases of
; CC   the cell cycle. The methods may be used to identify candidate drugs which
; CC   affect the cell cycle and for identification of antifungal drugs.
; CC   AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
; CC   the present invention. AAF33262 to AAF33267 represent linkers and PCR
; CC   primers used in the SAGE method, in the exemplification of the present
; CC   invention.
; XX
; SQ   Sequence 10 BP; 2 A; 1 C; 3 G; 4 T; 0 other;
;
;  AAF42631  Length: 10  October 2, 2003 14:58  Type: N  Check: 4071  ..
aaf42631

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3318 ATTCAGGG 3325
              ||||||||
Db          2 ATTCAGGG 9


RESULT 66
aaf42841/c
;  TOIG of: aaf42841  check: 4104  from: 1  to: 10
;
; ID   AAF42841 standard; DNA; 10 BP.
; XX
; AC   AAF42841;
; XX
; DT   23-MAR-2001  (first entry)
; XX
; DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:10980.
; XX
; KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
; KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
; KW   serial analysis of gene expression; antifungal; tag; identification;
; KW   linker; PCR primer; ds.
; XX
; OS   Saccharomyces cerevisiae.
; XX
; PN   WO200077214-A2.
; XX
```

; PD 21-DEC-2000.
; XX
; PF 14-JUN-2000; 2000WO-US16223.
; XX
; PR 16-JUN-1999; 99US-0335032.
; XX
; PA (UYJO) UNIV JOHNS HOPKINS.
; XX
; PI Velculescu V, Vogelstein B, Kinzler K;
; XX
; DR WPI; 2001-061874/07.
; XX
; PT Yeast gene coding sequences comprising NORF genes with serial analysis
; PT of gene expression (SAGE) tags, useful for studying, monitoring and
; PT affecting phases of the cell cycle -
; XX
; PS Example; Page 342; 419pp; English.
; XX
; CC The present invention describes an isolated DNA molecule comprising a
; CC coding sequence of a yeast gene selected from a group of 745 NORF (not
; CC previously assigned open reading frame; or nonannotated ORF) genes
; CC comprising a SAGE (serial analysis of gene expression) tag. Also
; CC described are: (1) a method (M1) of using NORF genes to affect the cell
; CC cycle comprising administering a NORF gene whose expression varies by at
; CC least 10% between any two phases of the cell cycle selected from log
; CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
; CC antifungal drugs comprising: (a) contacting a test substance with a
; CC yeast cell; and (b) monitoring expression of a NORF gene whose
; CC expression varies as in M1, where a test substance which modifies the
; CC expression of the yeast gene is a candidate antifungal drug; (3) a method
; CC (M3) for identifying human genes which are involved in cell cycle
; CC progression comprising contacting human DNA with a probe which comprises
; CC at least 10 contiguous nucleotides of a NORF gene whose expression varies
; CC as in M1; and (4) a method (M4) for identifying a candidate drug as a
; CC member of a class of drugs having a characteristic effect on gene
; CC expression in a yeast cell comprising contacting a yeast cell with a
; CC candidate drug and monitoring expression in the yeast cell of at least 1
; CC NORF gene whose expression is affected by the class of drugs. The NORF
; CC genes may be used to study, monitor and affect phases of the cell cycle,
; CC the differentially expressed genes may be used as markers of phases of
; CC the cell cycle. The methods may be used to identify candidate drugs which
; CC affect the cell cycle and for identification of antifungal drugs.
; CC AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
; CC the present invention. AAF33262 to AAF33267 represent linkers and PCR
; CC primers used in the SAGE method, in the exemplification of the present
; CC invention.
; XX
; SQ Sequence 10 BP; 2 A; 3 C; 1 G; 4 T; 0 other;
;
; AAF42841 Length: 10 October 2, 2003 14:58 Type: N Check: 4104 ..
aaf42841

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       3318 ATTCAGGG 3325
              ||||||||
Db          9 ATTCAGGG 2
```

RESULT 67
aah63748
; TOIG of: aah63748 check: 3877 from: 1 to: 10
;
; ID AAH63748 standard; cDNA; 10 BP.
; XX
; AC AAH63748;
; XX
; DT 20-SEP-2001 (first entry)
; XX
; DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 588.
; XX
; KW Human; transcriptome; gene expression pattern; cancer; drug screening;
; KW cancer diagnosis; cell specific gene expression; ss.
; XX
; OS Homo sapiens.
; XX
; PN WO200138577-A2.
; XX
; PD 31-MAY-2001.
; XX
; PF 21-NOV-2000; 2000WO-US31922.
; XX
; PR 24-NOV-1999; 99US-0448480.
; XX
; PA (UYJO) UNIV JOHNS HOPKINS.
; XX
; PI Velculescu VE, Vogelstein B, Kinzler KW;
; XX
; DR WPI; 2001-367706/38.
; XX
; PT New isolated polynucleotides, useful for identifying specific cell
; PT type, such as cancer cell, comprises transcriptomes expressed in
; PT particular cell types -
; XX
; PS Claim 13; Page 52; 94pp; English.
; XX
; CC The present invention describes a method of identifying the type of cell
; CC in a sample, involving determining which of the sequences
; CC AAH63161-AAH64724 is expressed by the cell. The transcriptomes described
; CC in the invention are cell-type specific, cancer specific or ubiquitously
; CC expressed in humans. They can also be used to screen for drugs, reduce
; CC cancer specific gene expression, standardise expression and restore the
; CC function of a diseased cell or tissue. The present sequence is one of
; CC the transcriptomes described in the exemplification of the invention.
; XX
; SQ Sequence 10 BP; 2 A; 1 C; 4 G; 3 T; 0 other;
;
; AAH63748 Length: 10 October 2, 2003 14:58 Type: N Check: 3877 ..
aah63748

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       3319 TTCAGGGG 3326
              ||||||||
Db          2 TTCAGGGG 9
```

RESULT 68
aaq63560
; TOIG of: aaq63560 check: 4214 from: 1 to: 10
;
; ID AAQ63560 standard; DNA; 10 BP.
; XX
; AC AAQ63560;
; XX
; DT 25-MAR-2003 (updated)
; DT 21-DEC-1994 (first entry)
; XX
; DE C8 3' spacer element.
; XX
; KW Insertion element; junk DNA; spacer element; functional DNA sequence;
; KW primer binding site; reaction product; binding specificity; primer;
; KW recombinant molecule; structural stress; hybridisation assay; ss.
; XX
; OS Synthetic.
; XX
; PN WO9409159-A2.
; XX
; PD 28-APR-1994.
; XX
; PF 08-OCT-1993; 93WO-US09702.
; XX

```
; PR   09-OCT-1992;   92US-0959939.
; PR   09-APR-1993;   93US-0045587.
; XX
; PA   (STAD ) AMOCO CORP.
; XX
; PI   Burg J;
; XX
; DR   WPI; 1994-151343/18.
; XX
; PT   Insertion elements and amplifiable nucleic acids - for use as
; PT   probes in hybridisation assays and for the prepn. of libraries
; PT   used to identify preferred insertion elements.
; XX
; PS   Disclosure; Page 23; 39pp; English.
; XX
; CC   The sequences given in AAQ63549-60 are spacer elements used within the
; CC   insertion elements of the invention. These insertion elements contain
; CC   junk DNA, two spacer elements, a functional DNA sequence and a
; CC   primer binding site. They also contain an MluI site, an MluI/NheI
; CC   site and a NheI site. The junk DNA serves to keep the MluI site
; CC   from being at the extreme emd of the molecule and also allows
; CC   determination that the MluI cleavage has occured because the extended
; CC   DNA will be reduced in size by the length of the junk sequence and
; CC   the junk sequence will appear as a reaction product. The
; CC   nucleotides making up the spacer elements are chosen randomly and
; CC   the functional nucleotide sequence is chosen to achieve the binding
; CC   specificity required of the amplifiable nucleic acid. The primer
; CC   binding site can be any nucleotide sequence for which a complementary
; CC   primer is available or can be synthesised. However, the primer and
; CC   primer binding site are chosen such that the primer itself does not
; CC   bind to any other portion of the insertion element under construction.
; CC   Insertion sequences such as these can be used to insert a functional
; CC   molecule into a host molecule to form a recombinant molecule. The
; CC   spacer elements are thought to relieve structural stresses imposed on
; CC   the host by addition of the functional nucleotide sequence. The
; CC   insertion elements can be used with nucleic acid hybridisation assays.
; CC   (Updated on 25-MAR-2003 to correct PN field.)
; XX
; SQ   Sequence 10 BP; 1 A; 1 C; 5 G; 3 T; 0 other;
;
;  AAQ63560  Length: 10  October 2, 2003 14:58  Type: N  Check: 4214  ..
aaq63560

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3321 CAGGGGTT 3328
              ||||||||
Db          1 CAGGGGTT 8


RESULT 69
aaz78096/c
;  TOIG of: aaz78096  check: 3984  from: 1  to: 10
;
; ID   AAZ78096 standard; DNA; 10 BP.
; XX
; AC   AAZ78096;
; XX
; DT   10-APR-2000  (first entry)
; XX
; DE   Human dendritic cell SAGE tag, SEQ ID NO:524.
; XX
; KW   SAGE tag; serial analysis of gene expression; antigen-presenting cell;
; KW   APC; monocyte-derived dendritic cell; differential gene expression;
; KW   immunostimulatory cofactor; costimulatory factor; CTL;
; KW   cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   WO9965924-A2.
; XX
; PD   23-DEC-1999.
; XX
; PF   18-JUN-1999;   99WO-US13800.
; XX
; PR   19-JUN-1998;   98US-0089833.
; PR   19-JUN-1998;   98US-0089844.
; PR   19-JUN-1998;   98US-0089853.
; PR   19-JUN-1998;   98US-0089878.
; PR   19-JUN-1998;   98US-0089991.
; PR   19-JUN-1998;   98US-0089992.
; PR   19-JUN-1998;   98US-0089993.
; PR   19-JUN-1998;   98US-0089994.
; PR   19-JUN-1998;   98US-0089997.
; PR   19-JUN-1998;   98US-0089999.
; PR   19-JUN-1998;   98US-0090000.
; PR   19-JUN-1998;   98US-0090035.
; PR   19-JUN-1998;   98US-0090036.
; PR   19-JUN-1998;   98US-0090039.
; PR   19-JUN-1998;   98US-0090040.
; PR   19-JUN-1998;   98US-0090041.
; PR   19-JUN-1998;   98US-0090042.
; PR   19-JUN-1998;   98US-0090043.
; PR   19-JUN-1998;   98US-0090044.
; PR   19-JUN-1998;   98US-0090045.
; PR   19-JUN-1998;   98US-0090047.
; PR   19-JUN-1998;   98US-0090048.
; PR   19-JUN-1998;   98US-0090072.
; PR   19-JUN-1998;   98US-0090076.
; PR   19-JUN-1998;   98US-0090077.
; PR   19-JUN-1998;   98US-0090078.
; PR   19-JUN-1998;   98US-0090079.
; PR   19-JUN-1998;   98US-0090080.
; PR   08-DEC-1998;   98US-0111715.
; XX
; PA   (GENZ ) GENZYME CORP.
; PA   (ROBE/) ROBERTS B L.
; PA   (SHAN/) SHANKARA S.
; XX
; PI   Roberts BL,  Shankara S;
; XX
; DR   WPI; 2000-106077/09.
; XX
; PT   Isolated polynucleotides differentially expressed in antigen-presenting
; PT   cells, useful in gene vaccines against cancer -
; XX
; PS   Claim 1; Page 80; 130pp; English.
; XX
; CC   Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
; CC   expression) tags used to identify mRNA transcripts encoding
; CC   immunostimulatory cofactor proteins which are preferentially or
; CC   differentially expressed in monocyte-derived dendritic cells compared
; CC   with monocytes. Some of the transcripts correspond to known genes or
; CC   ESTs (expressed sequence tags) which were previously unknown to be
; CC   preferentially or differentially expressed in dendritic cells, while
; CC   other transcripts correspond to novel genes. Antigen-presenting cell
; CC   (APC)-associated costimulatory factors play an important role in the
; CC   activation of the cytotoxic immune response, particularly against tumour
; CC   cells. Tumour antigen presentation via the MHC (major histocompatibility
; CC   complex) and subsequent recognition by T-cell receptors is alone
; CC   insufficient to activate a robust cytotoxic immune response that can
; CC   lyse the tumour cells, immunostimulatory cofactors also being required
; CC   for efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
; CC   sequences identified using the SAGE tags have several potential uses.
; CC   They may be used in vaccines to induce an immune response, particularly
; CC   against a tumour antigen; to modulate the genotype of an APC; to screen
; CC   for agents that modulate expression of differentially expressed genes in
; CC   an APC; and as hybridisation probes/amplification primers for the
; CC   diagnosis, prognosis and monitoring of diseases related to abnormal
; CC   expression of these genes. Detection of the dendritic cell
; CC   differentially expressed genes, or of their encoded proteins, can be used
; CC   to identify cells as belonging to the monocyte lineage. Cells containing
; CC   these genes can be used in active immunotherapy (or to stimulate
; CC   production of a population of antigen-specific effector cells) and
```

```
; CC   vectors containing them are used in gene therapy. Co-administration of
; CC   tumour antigens and APC-associated costimulatory factors ensures adequate
; CC   antigen presentation to endogenous APCs and upregulates the APCs for the
; CC   presentation of co-stimulatory signals, migration to T cell-rich sites,
; CC   secretion of T cell growth factors and secretion of chemokines for
; CC   recruitment of immune effector cells.
; XX
; SQ   Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 other;
;
;  AAZ78096  Length: 10  October 2, 2003 14:58  Type: N  Check: 3984  ..
aaz78096

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3320 TCAGGGGT 3327
              ||||||||
Db          9 TCAGGGGT 2


RESULT 70
aaz78337
;  TOIG of: aaz78337  check: 3934  from: 1  to: 10
;
; ID   AAZ78337 standard; DNA; 10 BP.
; XX
; AC   AAZ78337;
; XX
; DT   10-APR-2000  (first entry)
; XX
; DE   Human dendritic cell SAGE tag, SEQ ID NO:765.
; XX
; KW   SAGE tag; serial analysis of gene expression; antigen-presenting cell;
; KW   APC; monocyte-derived dendritic cell; differential gene expression;
; KW   immunostimulatory cofactor; costimulatory factor; CTL;
; KW   cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   WO9965924-A2.
; XX
; PD   23-DEC-1999.
; XX
; PF   18-JUN-1999;   99WO-US13800.
; XX
; PR   19-JUN-1998;   98US-0089833.
; PR   19-JUN-1998;   98US-0089844.
; PR   19-JUN-1998;   98US-0089853.
; PR   19-JUN-1998;   98US-0089878.
; PR   19-JUN-1998;   98US-0089991.
; PR   19-JUN-1998;   98US-0089992.
; PR   19-JUN-1998;   98US-0089993.
; PR   19-JUN-1998;   98US-0089994.
; PR   19-JUN-1998;   98US-0089997.
; PR   19-JUN-1998;   98US-0089999.
; PR   19-JUN-1998;   98US-0090000.
; PR   19-JUN-1998;   98US-0090035.
; PR   19-JUN-1998;   98US-0090036.
; PR   19-JUN-1998;   98US-0090039.
; PR   19-JUN-1998;   98US-0090040.
; PR   19-JUN-1998;   98US-0090041.
; PR   19-JUN-1998;   98US-0090042.
; PR   19-JUN-1998;   98US-0090043.
; PR   19-JUN-1998;   98US-0090044.
; PR   19-JUN-1998;   98US-0090045.
; PR   19-JUN-1998;   98US-0090047.
; PR   19-JUN-1998;   98US-0090048.
; PR   19-JUN-1998;   98US-0090072.
; PR   19-JUN-1998;   98US-0090076.
; PR   19-JUN-1998;   98US-0090077.
; PR   19-JUN-1998;   98US-0090078.
; PR   19-JUN-1998;   98US-0090079.
; PR   19-JUN-1998;   98US-0090080.
; PR   08-DEC-1998;   98US-0111715.
; XX
; PA   (GENZ ) GENZYME CORP.
; PA   (ROBE/) ROBERTS B L.
; PA   (SHAN/) SHANKARA S.
; XX
; PI   Roberts BL,  Shankara S;
; XX
; DR   WPI; 2000-106077/09.
; XX
; PT   Isolated polynucleotides differentially expressed in antigen-presenting
; PT   cells, useful in gene vaccines against cancer -
; XX
; PS   Claim 1; Page 87; 130pp; English.
; XX
; CC   Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
; CC   expression) tags used to identify mRNA transcripts encoding
; CC   immunostimulatory cofactor proteins which are preferentially or
; CC   differentially expressed in monocyte-derived dendritic cells compared
; CC   with monocytes. Some of the transcripts correspond to known genes or
; CC   ESTs (expressed sequence tags) which were previously unknown to be
; CC   preferentially or differentially expressed in dendritic cells, while
; CC   other transcripts correspond to novel genes. Antigen-presenting cell
; CC   (APC)-associated costimulatory factors play an important role in the
; CC   activation of the cytotoxic immune response, particularly against tumour
; CC   cells. Tumour antigen presentation via the MHC (major histocompatibility
; CC   complex) and subsequent recognition by T-cell receptors is alone
; CC   insufficient to activate a robust cytotoxic immune response that can
; CC   lyse the tumour cells, immunostimulatory cofactors also being required
; CC   for efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
; CC   sequences identified using the SAGE tags have several potential uses.
; CC   They may be used in vaccines to induce an immune response, particularly
; CC   against a tumour antigen; to modulate the genotype of an APC; to screen
; CC   for agents that modulate expression of differentially expressed genes in
; CC   an APC; and as hybridisation probes/amplification primers for the
; CC   diagnosis, prognosis and monitoring of diseases related to abnormal
; CC   expression of these genes. Detection of the dendritic cell
; CC   differentially expressed genes, or of their encoded proteins, can be used
; CC   to identify cells as belonging to the monocyte lineage. Cells containing
; CC   these genes can be used in active immunotherapy (or to stimulate
; CC   production of a population of antigen-specific effector cells) and
; CC   vectors containing them are used in gene therapy. Co-administration of
; CC   tumour antigens and APC-associated costimulatory factors ensures adequate
; CC   antigen presentation to endogenous APCs and upregulates the APCs for the
; CC   presentation of co-stimulatory signals, migration to T cell-rich sites,
; CC   secretion of T cell growth factors and secretion of chemokines for
; CC   recruitment of immune effector cells.
; XX
; SQ   Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 other;
;
;  AAZ78337  Length: 10  October 2, 2003 14:58  Type: N  Check: 3934  ..
aaz78337

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3324 GGGTTCCA 3331
              ||||||||
Db          3 GGGTTCCA 10


RESULT 71
aaz78909
;  TOIG of: aaz78909  check: 3877  from: 1  to: 10
;
; ID   AAZ78909 standard; DNA; 10 BP.
; XX
; AC   AAZ78909;
; XX
; DT   10-APR-2000  (first entry)
; XX
```

```
; DE   Human dendritic cell SAGE tag, SEQ ID NO:1337.
; XX
; KW   SAGE tag; serial analysis of gene expression; antigen-presenting cell;
; KW   APC; monocyte-derived dendritic cell; differential gene expression;
; KW   immunostimulatory cofactor; costimulatory factor; CTL;
; KW   cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   WO9965924-A2.
; XX
; PD   23-DEC-1999.
; XX
; PF   18-JUN-1999;   99WO-US13800.
; XX
; PR   19-JUN-1998;   98US-0089833.
; PR   19-JUN-1998;   98US-0089844.
; PR   19-JUN-1998;   98US-0089853.
; PR   19-JUN-1998;   98US-0089878.
; PR   19-JUN-1998;   98US-0089991.
; PR   19-JUN-1998;   98US-0089992.
; PR   19-JUN-1998;   98US-0089993.
; PR   19-JUN-1998;   98US-0089994.
; PR   19-JUN-1998;   98US-0089997.
; PR   19-JUN-1998;   98US-0089999.
; PR   19-JUN-1998;   98US-0090000.
; PR   19-JUN-1998;   98US-0090035.
; PR   19-JUN-1998;   98US-0090036.
; PR   19-JUN-1998;   98US-0090039.
; PR   19-JUN-1998;   98US-0090040.
; PR   19-JUN-1998;   98US-0090041.
; PR   19-JUN-1998;   98US-0090042.
; PR   19-JUN-1998;   98US-0090043.
; PR   19-JUN-1998;   98US-0090044.
; PR   19-JUN-1998;   98US-0090045.
; PR   19-JUN-1998;   98US-0090047.
; PR   19-JUN-1998;   98US-0090048.
; PR   19-JUN-1998;   98US-0090072.
; PR   19-JUN-1998;   98US-0090076.
; PR   19-JUN-1998;   98US-0090077.
; PR   19-JUN-1998;   98US-0090078.
; PR   19-JUN-1998;   98US-0090079.
; PR   19-JUN-1998;   98US-0090080.
; PR   08-DEC-1998;   98US-0111715.
; XX
; PA   (GENZ ) GENZYME CORP.
; PA   (ROBE/) ROBERTS B L.
; PA   (SHAN/) SHANKARA S.
; XX
; PI   Roberts BL,  Shankara S;
; XX
; DR   WPI; 2000-106077/09.
; XX
; PT   Isolated polynucleotides differentially expressed in antigen-presenting
; PT   cells, useful in gene vaccines against cancer -
; XX
; PS   Claim 1; Page 103; 130pp; English.
; XX
; CC   Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
; CC   expression) tags used to identify mRNA transcripts encoding
; CC   immunostimulatory cofactor proteins which are preferentially or
; CC   differentially expressed in monocyte-derived dendritic cells compared
; CC   with monocytes. Some of the transcripts correspond to known genes or
; CC   ESTs (expressed sequence tags) which were previously unknown to be
; CC   preferentially or differentially expressed in dendritic cells, while
; CC   other transcripts correspond to novel genes. Antigen-presenting cell
; CC   (APC)-associated costimulatory factors play an important role in the
; CC   activation of the cytotoxic immune response, particularly against tumour
; CC   cells. Tumour antigen presentation via the MHC (major histocompatibility
; CC   complex) and subsequent recognition by T-cell receptors is alone
; CC   insufficient to activate a robust cytotoxic immune response that can
; CC   lyse the tumour cells, immunostimulatory cofactors also being required
; CC   for efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
; CC   sequences identified using the SAGE tags have several potential uses.
; CC   They may be used in vaccines to induce an immune response, particularly
; CC   against a tumour antigen; to modulate the genotype of an APC; to screen
; CC   for agents that modulate expression of differentially expressed genes in
; CC   an APC; and as hybridisation probes/amplification primers for the
; CC   diagnosis, prognosis and monitoring of diseases related to abnormal
; CC   expression of these genes. Detection of the dendritic cell
; CC   differentially expressed genes, or of their encoded proteins, can be used
; CC   to identify cells as belonging to the monocyte lineage. Cells containing
; CC   these genes can be used in active immunotherapy (or to stimulate
; CC   production of a population of antigen-specific effector cells) and
; CC   vectors containing them are used in gene therapy. Co-administration of
; CC   tumour antigens and APC-associated costimulatory factors ensures adequate
; CC   antigen presentation to endogenous APCs and upregulates the APCs for the
; CC   presentation of co-stimulatory signals, migration to T cell-rich sites,
; CC   secretion of T cell growth factors and secretion of chemokines for
; CC   recruitment of immune effector cells.
; XX
; SQ   Sequence 10 BP; 2 A; 1 C; 4 G; 3 T; 0 other;
;
;  AAZ78909  Length: 10  October 2, 2003 14:58  Type: N  Check: 3877  ..
aaz78909

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3319 TTCAGGGG 3326
              ||||||||
Db          2 TTCAGGGG 9


RESULT 72
aaz81683/c
;  TOIG of: aaz81683  check: 3813  from: 1  to: 10
;
; ID   AAZ81683 standard; DNA; 10 BP.
; XX
; AC   AAZ81683;
; XX
; DT   07-APR-2000  (first entry)
; XX
; DE   Metastatic breast tumour cell upregulated transcript tag #917.
; XX
; KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
; KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
; KW   antimetastatic; vaccine; diagnosis; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   WO9965928-A2.
; XX
; PD   23-DEC-1999.
; XX
; PF   18-JUN-1999;   99WO-US13647.
; XX
; PR   19-JUN-1998;   98US-0089853.
; PR   19-JUN-1998;   98US-0089997.
; PR   19-JUN-1998;   98US-0090039.
; PR   19-JUN-1998;   98US-0090040.
; PR   19-JUN-1998;   98US-0090041.
; XX
; PA   (GENZ ) GENZYME CORP.
; PA   (ROBE/) ROBERTS B L.
; PA   (SHAN/) SHANKARA S.
; XX
; PI   Roberts BL,  Shankara S;
; XX
; DR   WPI; 2000-106079/09.
; XX
; PT   Isolated polynucleotides differentially expressed between metastatic
; PT   and non-metastatic breast cancer cells, useful for diagnosis,
; PT   prevention and treatment of cancer -
```

```
; XX
; PS   Claim 1; Page 83; 219pp; English.
; XX
; CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
; CC   transcripts that are preferentially transcribed in the metastatic breast
; CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
; CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
; CC   that are preferentially transcribed in the primary or non-metastatic
; CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
; CC   cells). These transcripts can be used for diagnosis, prognosis,
; CC   monitoring and treatment of breast cancer, particularly where metastatic.
; CC   Diagnosis is by standard immunoassays or hybridisation/amplification
; CC   reactions. Compounds that modulate expression of the transcripts are
; CC   potentially useful for treatment of (metastatic) breast cancer, while
; CC   promoters from the transcripts are used to direct expression, in selected
; CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
; CC   sequences), particularly an antigen-encoding sequence for use in gene or
; CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
; CC   useful in vaccines; for diagnosing breast cancer and for raising
; CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
; CC   therapeutic agents. Host cells that produce the polypeptides can be used
; CC   to expand and isolate populations of educated, antigen-specific immune
; CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
; CC   adoptive immunotherapy.
; XX
; SQ   Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 other;
;
;  AAZ81683  Length: 10  October 2, 2003 14:58  Type: N  Check: 3813  ..
aaz81683

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3320 TCAGGGGT 3327
              ||||||||
Db          8 TCAGGGGT 1


RESULT 73
aaz82371/c
;  TOIG of: aaz82371  check: 3984  from: 1  to: 10
;
; ID   AAZ82371 standard; DNA; 10 BP.
; XX
; AC   AAZ82371;
; XX
; DT   07-APR-2000  (first entry)
; XX
; DE   Metastatic breast tumour cell upregulated transcript tag #1605.
; XX
; KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
; KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
; KW   antimetastatic; vaccine; diagnosis; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   WO9965928-A2.
; XX
; PD   23-DEC-1999.
; XX
; PF   18-JUN-1999;   99WO-US13647.
; XX
; PR   19-JUN-1998;   98US-0089853.
; PR   19-JUN-1998;   98US-0089997.
; PR   19-JUN-1998;   98US-0090039.
; PR   19-JUN-1998;   98US-0090040.
; PR   19-JUN-1998;   98US-0090041.
; XX
; PA   (GENZ ) GENZYME CORP.
; PA   (ROBE/) ROBERTS B L.
; PA   (SHAN/) SHANKARA S.
; XX
; PI   Roberts BL,  Shankara S;
; XX
; DR   WPI; 2000-106079/09.
; XX
; PT   Isolated polynucleotides differentially expressed between metastatic
; PT   and non-metastatic breast cancer cells, useful for diagnosis,
; PT   prevention and treatment of cancer -
; XX
; PS   Claim 1; Page 101; 219pp; English.
; XX
; CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
; CC   transcripts that are preferentially transcribed in the metastatic breast
; CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
; CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
; CC   that are preferentially transcribed in the primary or non-metastatic
; CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
; CC   cells). These transcripts can be used for diagnosis, prognosis,
; CC   monitoring and treatment of breast cancer, particularly where metastatic.
; CC   Diagnosis is by standard immunoassays or hybridisation/amplification
; CC   reactions. Compounds that modulate expression of the transcripts are
; CC   potentially useful for treatment of (metastatic) breast cancer, while
; CC   promoters from the transcripts are used to direct expression, in selected
; CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
; CC   sequences), particularly an antigen-encoding sequence for use in gene or
; CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
; CC   useful in vaccines; for diagnosing breast cancer and for raising
; CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
; CC   therapeutic agents. Host cells that produce the polypeptides can be used
; CC   to expand and isolate populations of educated, antigen-specific immune
; CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
; CC   adoptive immunotherapy.
; XX
; SQ   Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 other;
;
;  AAZ82371  Length: 10  October 2, 2003 14:58  Type: N  Check: 3984  ..
aaz82371

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3320 TCAGGGGT 3327
              ||||||||
Db          9 TCAGGGGT 2


RESULT 74
aaz83968/c
;  TOIG of: aaz83968  check: 3832  from: 1  to: 10
;
; ID   AAZ83968 standard; DNA; 10 BP.
; XX
; AC   AAZ83968;
; XX
; DT   07-APR-2000  (first entry)
; XX
; DE   Metastatic breast tumour cell downregulated transcript tag #3202.
; XX
; KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
; KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
; KW   antimetastatic; vaccine; diagnosis; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   WO9965928-A2.
; XX
; PD   23-DEC-1999.
; XX
; PF   18-JUN-1999;   99WO-US13647.
; XX
; PR   19-JUN-1998;   98US-0089853.
; PR   19-JUN-1998;   98US-0089997.
; PR   19-JUN-1998;   98US-0090039.
```

```
; PR   19-JUN-1998;   98US-0090040.
; PR   19-JUN-1998;   98US-0090041.
; XX
; PA   (GENZ ) GENZYME CORP.
; PA   (ROBE/) ROBERTS B L.
; PA   (SHAN/) SHANKARA S.
; XX
; PI   Roberts BL,  Shankara S;
; XX
; DR   WPI; 2000-106079/09.
; XX
; PT   Isolated polynucleotides differentially expressed between metastatic
; PT   and non-metastatic breast cancer cells, useful for diagnosis,
; PT   prevention and treatment of cancer -
; XX
; PS   Claim 1; Page 144; 219pp; English.
; XX
; CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
; CC   transcripts that are preferentially transcribed in the metastatic breast
; CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
; CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
; CC   that are preferentially transcribed in the primary or non-metastatic
; CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
; CC   cells). These transcripts can be used for diagnosis, prognosis,
; CC   monitoring and treatment of breast cancer, particularly where metastatic.
; CC   Diagnosis is by standard immunoassays or hybridisation/amplification
; CC   reactions. Compounds that modulate expression of the transcripts are
; CC   potentially useful for treatment of (metastatic) breast cancer, while
; CC   promoters from the transcripts are used to direct expression, in selected
; CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
; CC   sequences), particularly an antigen-encoding sequence for use in gene or
; CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
; CC   useful in vaccines; for diagnosing breast cancer and for raising
; CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
; CC   therapeutic agents. Host cells that produce the polypeptides can be used
; CC   to expand and isolate populations of educated, antigen-specific immune
; CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
; CC   adoptive immunotherapy.
; XX
; SQ   Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 other;
;
;  AAZ83968  Length: 10  October 2, 2003 14:58  Type: N  Check: 3832  ..
aaz83968

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3315 GGGATTCA 3322
              ||||||||
Db          9 GGGATTCA 2


RESULT 75
aaz84127
;  TOIG of: aaz84127  check: 3934  from: 1  to: 10
;
; ID   AAZ84127 standard; DNA; 10 BP.
; XX
; AC   AAZ84127;
; XX
; DT   07-APR-2000  (first entry)
; XX
; DE   Metastatic breast tumour cell downregulated transcript tag #3361.
; XX
; KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
; KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
; KW   antimetastatic; vaccine; diagnosis; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   WO9965928-A2.
; XX
; PD   23-DEC-1999.
; XX
; PF   18-JUN-1999;   99WO-US13647.
; XX
; PR   19-JUN-1998;   98US-0089853.
; PR   19-JUN-1998;   98US-0089997.
; PR   19-JUN-1998;   98US-0090039.
; PR   19-JUN-1998;   98US-0090040.
; PR   19-JUN-1998;   98US-0090041.
; XX
; PA   (GENZ ) GENZYME CORP.
; PA   (ROBE/) ROBERTS B L.
; PA   (SHAN/) SHANKARA S.
; XX
; PI   Roberts BL,  Shankara S;
; XX
; DR   WPI; 2000-106079/09.
; XX
; PT   Isolated polynucleotides differentially expressed between metastatic
; PT   and non-metastatic breast cancer cells, useful for diagnosis,
; PT   prevention and treatment of cancer -
; XX
; PS   Claim 1; Page 149; 219pp; English.
; XX
; CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
; CC   transcripts that are preferentially transcribed in the metastatic breast
; CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
; CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
; CC   that are preferentially transcribed in the primary or non-metastatic
; CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
; CC   cells). These transcripts can be used for diagnosis, prognosis,
; CC   monitoring and treatment of breast cancer, particularly where metastatic.
; CC   Diagnosis is by standard immunoassays or hybridisation/amplification
; CC   reactions. Compounds that modulate expression of the transcripts are
; CC   potentially useful for treatment of (metastatic) breast cancer, while
; CC   promoters from the transcripts are used to direct expression, in selected
; CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
; CC   sequences), particularly an antigen-encoding sequence for use in gene or
; CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
; CC   useful in vaccines; for diagnosing breast cancer and for raising
; CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
; CC   therapeutic agents. Host cells that produce the polypeptides can be used
; CC   to expand and isolate populations of educated, antigen-specific immune
; CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
; CC   adoptive immunotherapy.
; XX
; SQ   Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 other;
;
;  AAZ84127  Length: 10  October 2, 2003 14:58  Type: N  Check: 3934  ..
aaz84127

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3324 GGGTTCCA 3331
              ||||||||
Db          3 GGGTTCCA 10


RESULT 76
aaz84157
;  TOIG of: aaz84157  check: 3812  from: 1  to: 10
;
; ID   AAZ84157 standard; DNA; 10 BP.
; XX
; AC   AAZ84157;
; XX
; DT   07-APR-2000  (first entry)
; XX
; DE   Metastatic breast tumour cell downregulated transcript tag #3391.
; XX
; KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
```

```
; KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
; KW   antimetastatic; vaccine; diagnosis; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   WO9965928-A2.
; XX
; PD   23-DEC-1999.
; XX
; PF   18-JUN-1999;   99WO-US13647.
; XX
; PR   19-JUN-1998;   98US-0089853.
; PR   19-JUN-1998;   98US-0089997.
; PR   19-JUN-1998;   98US-0090039.
; PR   19-JUN-1998;   98US-0090040.
; PR   19-JUN-1998;   98US-0090041.
; XX
; PA   (GENZ ) GENZYME CORP.
; PA   (ROBE/) ROBERTS B L.
; PA   (SHAN/) SHANKARA S.
; XX
; PI   Roberts BL,  Shankara S;
; XX
; DR   WPI; 2000-106079/09.
; XX
; PT   Isolated polynucleotides differentially expressed between metastatic
; PT   and non-metastatic breast cancer cells, useful for diagnosis,
; PT   prevention and treatment of cancer -
; XX
; PS   Claim 1; Page 149; 219pp; English.
; XX
; CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
; CC   transcripts that are preferentially transcribed in the metastatic breast
; CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
; CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
; CC   that are preferentially transcribed in the primary or non-metastatic
; CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
; CC   cells). These transcripts can be used for diagnosis, prognosis,
; CC   monitoring and treatment of breast cancer, particularly where metastatic.
; CC   Diagnosis is by standard immunoassays or hybridisation/amplification
; CC   reactions. Compounds that modulate expression of the transcripts are
; CC   potentially useful for treatment of (metastatic) breast cancer, while
; CC   promoters from the transcripts are used to direct expression, in selected
; CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
; CC   sequences), particularly an antigen-encoding sequence for use in gene or
; CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
; CC   useful in vaccines; for diagnosing breast cancer and for raising
; CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
; CC   therapeutic agents. Host cells that produce the polypeptides can be used
; CC   to expand and isolate populations of educated, antigen-specific immune
; CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
; CC   adoptive immunotherapy.
; XX
; SQ   Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 other;
;
;  AAZ84157  Length: 10  October 2, 2003 14:58  Type: N  Check: 3812  ..
aaz84157

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3326 GTTCCAGC 3333
              ||||||||
Db          1 GTTCCAGC 8


RESULT 77
aaz84158/c
;  TOIG of: aaz84158  check: 3703  from: 1  to: 10
;
; ID   AAZ84158 standard; DNA; 10 BP.
; XX
; AC   AAZ84158;
; XX
; DT   07-APR-2000  (first entry)
; XX
; DE   Metastatic breast tumour cell downregulated transcript tag #3392.
; XX
; KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
; KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
; KW   antimetastatic; vaccine; diagnosis; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   WO9965928-A2.
; XX
; PD   23-DEC-1999.
; XX
; PF   18-JUN-1999;   99WO-US13647.
; XX
; PR   19-JUN-1998;   98US-0089853.
; PR   19-JUN-1998;   98US-0089997.
; PR   19-JUN-1998;   98US-0090039.
; PR   19-JUN-1998;   98US-0090040.
; PR   19-JUN-1998;   98US-0090041.
; XX
; PA   (GENZ ) GENZYME CORP.
; PA   (ROBE/) ROBERTS B L.
; PA   (SHAN/) SHANKARA S.
; XX
; PI   Roberts BL,  Shankara S;
; XX
; DR   WPI; 2000-106079/09.
; XX
; PT   Isolated polynucleotides differentially expressed between metastatic
; PT   and non-metastatic breast cancer cells, useful for diagnosis,
; PT   prevention and treatment of cancer -
; XX
; PS   Claim 1; Page 149; 219pp; English.
; XX
; CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
; CC   transcripts that are preferentially transcribed in the metastatic breast
; CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
; CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
; CC   that are preferentially transcribed in the primary or non-metastatic
; CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
; CC   cells). These transcripts can be used for diagnosis, prognosis,
; CC   monitoring and treatment of breast cancer, particularly where metastatic.
; CC   Diagnosis is by standard immunoassays or hybridisation/amplification
; CC   reactions. Compounds that modulate expression of the transcripts are
; CC   potentially useful for treatment of (metastatic) breast cancer, while
; CC   promoters from the transcripts are used to direct expression, in selected
; CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
; CC   sequences), particularly an antigen-encoding sequence for use in gene or
; CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
; CC   useful in vaccines; for diagnosing breast cancer and for raising
; CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
; CC   therapeutic agents. Host cells that produce the polypeptides can be used
; CC   to expand and isolate populations of educated, antigen-specific immune
; CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
; CC   adoptive immunotherapy.
; XX
; SQ   Sequence 10 BP; 4 A; 3 C; 2 G; 1 T; 0 other;
;
;  AAZ84158  Length: 10  October 2, 2003 14:58  Type: N  Check: 3703  ..
aaz84158

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3324 GGGTTCCA 3331
              ||||||||
Db          9 GGGTTCCA 2
```

```
RESULT 78
aaz84257/c
;  TOIG of: aaz84257  check: 4042  from: 1  to: 10
;
; ID   AAZ84257 standard; DNA; 10 BP.
; XX
; AC   AAZ84257;
; XX
; DT   07-APR-2000  (first entry)
; XX
; DE   Metastatic breast tumour cell downregulated transcript tag #3491.
; XX
; KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
; KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
; KW   antimetastatic; vaccine; diagnosis; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   WO9965928-A2.
; XX
; PD   23-DEC-1999.
; XX
; PF   18-JUN-1999;   99WO-US13647.
; XX
; PR   19-JUN-1998;   98US-0089853.
; PR   19-JUN-1998;   98US-0089997.
; PR   19-JUN-1998;   98US-0090039.
; PR   19-JUN-1998;   98US-0090040.
; PR   19-JUN-1998;   98US-0090041.
; XX
; PA   (GENZ ) GENZYME CORP.
; PA   (ROBE/) ROBERTS B L.
; PA   (SHAN/) SHANKARA S.
; XX
; PI   Roberts BL,  Shankara S;
; XX
; DR   WPI; 2000-106079/09.
; XX
; PT   Isolated polynucleotides differentially expressed between metastatic
; PT   and non-metastatic breast cancer cells, useful for diagnosis,
; PT   prevention and treatment of cancer -
; XX
; PS   Claim 1; Page 152; 219pp; English.
; XX
; CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
; CC   transcripts that are preferentially transcribed in the metastatic breast
; CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
; CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
; CC   that are preferentially transcribed in the primary or non-metastatic
; CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
; CC   cells). These transcripts can be used for diagnosis, prognosis,
; CC   monitoring and treatment of breast cancer, particularly where metastatic.
; CC   Diagnosis is by standard immunoassays or hybridisation/amplification
; CC   reactions. Compounds that modulate expression of the transcripts are
; CC   potentially useful for treatment of (metastatic) breast cancer, while
; CC   promoters from the transcripts are used to direct expression, in selected
; CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
; CC   sequences), particularly an antigen-encoding sequence for use in gene or
; CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
; CC   useful in vaccines; for diagnosing breast cancer and for raising
; CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
; CC   therapeutic agents. Host cells that produce the polypeptides can be used
; CC   to expand and isolate populations of educated, antigen-specific immune
; CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
; CC   adoptive immunotherapy.
; XX
; SQ   Sequence 10 BP; 2 A; 3 C; 2 G; 3 T; 0 other;
;
;  AAZ84257  Length: 10  October 2, 2003 14:58  Type: N  Check: 4042  ..
aaz84257

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3317 GATTCAGG 3324
              ||||||||
Db          8 GATTCAGG 1


RESULT 79
aaz84401/c
;  TOIG of: aaz84401  check: 3887  from: 1  to: 10
;
; ID   AAZ84401 standard; DNA; 10 BP.
; XX
; AC   AAZ84401;
; XX
; DT   07-APR-2000  (first entry)
; XX
; DE   Metastatic breast tumour cell downregulated transcript tag #3635.
; XX
; KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
; KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
; KW   antimetastatic; vaccine; diagnosis; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   WO9965928-A2.
; XX
; PD   23-DEC-1999.
; XX
; PF   18-JUN-1999;   99WO-US13647.
; XX
; PR   19-JUN-1998;   98US-0089853.
; PR   19-JUN-1998;   98US-0089997.
; PR   19-JUN-1998;   98US-0090039.
; PR   19-JUN-1998;   98US-0090040.
; PR   19-JUN-1998;   98US-0090041.
; XX
; PA   (GENZ ) GENZYME CORP.
; PA   (ROBE/) ROBERTS B L.
; PA   (SHAN/) SHANKARA S.
; XX
; PI   Roberts BL,  Shankara S;
; XX
; DR   WPI; 2000-106079/09.
; XX
; PT   Isolated polynucleotides differentially expressed between metastatic
; PT   and non-metastatic breast cancer cells, useful for diagnosis,
; PT   prevention and treatment of cancer -
; XX
; PS   Claim 1; Page 156; 219pp; English.
; XX
; CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
; CC   transcripts that are preferentially transcribed in the metastatic breast
; CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
; CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
; CC   that are preferentially transcribed in the primary or non-metastatic
; CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
; CC   cells). These transcripts can be used for diagnosis, prognosis,
; CC   monitoring and treatment of breast cancer, particularly where metastatic.
; CC   Diagnosis is by standard immunoassays or hybridisation/amplification
; CC   reactions. Compounds that modulate expression of the transcripts are
; CC   potentially useful for treatment of (metastatic) breast cancer, while
; CC   promoters from the transcripts are used to direct expression, in selected
; CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
; CC   sequences), particularly an antigen-encoding sequence for use in gene or
; CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
; CC   useful in vaccines; for diagnosing breast cancer and for raising
; CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
; CC   therapeutic agents. Host cells that produce the polypeptides can be used
; CC   to expand and isolate populations of educated, antigen-specific immune
; CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
; CC   adoptive immunotherapy.
```

```
; XX
; SQ   Sequence 10 BP; 2 A; 4 C; 2 G; 2 T; 0 other;
;
;  AAZ84401  Length: 10  October 2, 2003 14:58  Type: N  Check: 3887  ..
aaz84401

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3322 AGGGGTTC 3329
              ||||||||
Db         10 AGGGGTTC 3


RESULT 80
aaz84685
;  TOIG of: aaz84685  check: 4063  from: 1  to: 10
;
; ID   AAZ84685 standard; DNA; 10 BP.
; XX
; AC   AAZ84685;
; XX
; DT   07-APR-2000  (first entry)
; XX
; DE   Metastatic breast tumour cell downregulated transcript tag #3919.
; XX
; KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
; KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
; KW   antimetastatic; vaccine; diagnosis; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   WO9965928-A2.
; XX
; PD   23-DEC-1999.
; XX
; PF   18-JUN-1999;   99WO-US13647.
; XX
; PR   19-JUN-1998;   98US-0089853.
; PR   19-JUN-1998;   98US-0089997.
; PR   19-JUN-1998;   98US-0090039.
; PR   19-JUN-1998;   98US-0090040.
; PR   19-JUN-1998;   98US-0090041.
; XX
; PA   (GENZ ) GENZYME CORP.
; PA   (ROBE/) ROBERTS B L.
; PA   (SHAN/) SHANKARA S.
; XX
; PI   Roberts BL,  Shankara S;
; XX
; DR   WPI; 2000-106079/09.
; XX
; PT   Isolated polynucleotides differentially expressed between metastatic
; PT   and non-metastatic breast cancer cells, useful for diagnosis,
; PT   prevention and treatment of cancer -
; XX
; PS   Claim 1; Page 163; 219pp; English.
; XX
; CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
; CC   transcripts that are preferentially transcribed in the metastatic breast
; CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
; CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
; CC   that are preferentially transcribed in the primary or non-metastatic
; CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
; CC   cells). These transcripts can be used for diagnosis, prognosis,
; CC   monitoring and treatment of breast cancer, particularly where metastatic.
; CC   Diagnosis is by standard immunoassays or hybridisation/amplification
; CC   reactions. Compounds that modulate expression of the transcripts are
; CC   potentially useful for treatment of (metastatic) breast cancer, while
; CC   promoters from the transcripts are used to direct expression, in selected
; CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
; CC   sequences), particularly an antigen-encoding sequence for use in gene or
; CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
; CC   useful in vaccines; for diagnosing breast cancer and for raising
; CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
; CC   therapeutic agents. Host cells that produce the polypeptides can be used
; CC   to expand and isolate populations of educated, antigen-specific immune
; CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
; CC   adoptive immunotherapy.
; XX
; SQ   Sequence 10 BP; 0 A; 2 C; 4 G; 4 T; 0 other;
;
;  AAZ84685  Length: 10  October 2, 2003 14:58  Type: N  Check: 4063  ..
aaz84685

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3323 GGGGTTCC 3330
              ||||||||
Db          3 GGGGTTCC 10


RESULT 81
aaz85131
;  TOIG of: aaz85131  check: 3877  from: 1  to: 10
;
; ID   AAZ85131 standard; DNA; 10 BP.
; XX
; AC   AAZ85131;
; XX
; DT   07-APR-2000  (first entry)
; XX
; DE   Metastatic breast tumour cell downregulated transcript tag #4365.
; XX
; KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
; KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
; KW   antimetastatic; vaccine; diagnosis; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   WO9965928-A2.
; XX
; PD   23-DEC-1999.
; XX
; PF   18-JUN-1999;   99WO-US13647.
; XX
; PR   19-JUN-1998;   98US-0089853.
; PR   19-JUN-1998;   98US-0089997.
; PR   19-JUN-1998;   98US-0090039.
; PR   19-JUN-1998;   98US-0090040.
; PR   19-JUN-1998;   98US-0090041.
; XX
; PA   (GENZ ) GENZYME CORP.
; PA   (ROBE/) ROBERTS B L.
; PA   (SHAN/) SHANKARA S.
; XX
; PI   Roberts BL,  Shankara S;
; XX
; DR   WPI; 2000-106079/09.
; XX
; PT   Isolated polynucleotides differentially expressed between metastatic
; PT   and non-metastatic breast cancer cells, useful for diagnosis,
; PT   prevention and treatment of cancer -
; XX
; PS   Claim 1; Page 176; 219pp; English.
; XX
; CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
; CC   transcripts that are preferentially transcribed in the metastatic breast
; CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
; CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
; CC   that are preferentially transcribed in the primary or non-metastatic
; CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
; CC   cells). These transcripts can be used for diagnosis, prognosis,
```

```
; CC   monitoring and treatment of breast cancer, particularly where metastatic.
; CC   Diagnosis is by standard immunoassays or hybridisation/amplification
; CC   reactions. Compounds that modulate expression of the transcripts are
; CC   potentially useful for treatment of (metastatic) breast cancer, while
; CC   promoters from the transcripts are used to direct expression, in selected
; CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
; CC   sequences), particularly an antigen-encoding sequence for use in gene or
; CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
; CC   useful in vaccines; for diagnosing breast cancer and for raising
; CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
; CC   therapeutic agents. Host cells that produce the polypeptides can be used
; CC   to expand and isolate populations of educated, antigen-specific immune
; CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
; CC   adoptive immunotherapy.
; XX
; SQ   Sequence 10 BP; 2 A; 1 C; 4 G; 3 T; 0 other;
;
;  AAZ85131  Length: 10  October 2, 2003 14:58  Type: N  Check: 3877  ..
aaz85131

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3319 TTCAGGGG 3326
              ||||||||
Db          2 TTCAGGGG 9


RESULT 82
aaz85236/c
;  TOIG of: aaz85236  check: 3825  from: 1  to: 10
;
; ID   AAZ85236 standard; DNA; 10 BP.
; XX
; AC   AAZ85236;
; XX
; DT   07-APR-2000  (first entry)
; XX
; DE   Metastatic breast tumour cell downregulated transcript tag #4470.
; XX
; KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
; KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
; KW   antimetastatic; vaccine; diagnosis; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   WO9965928-A2.
; XX
; PD   23-DEC-1999.
; XX
; PF   18-JUN-1999;   99WO-US13647.
; XX
; PR   19-JUN-1998;   98US-0089853.
; PR   19-JUN-1998;   98US-0089997.
; PR   19-JUN-1998;   98US-0090039.
; PR   19-JUN-1998;   98US-0090040.
; PR   19-JUN-1998;   98US-0090041.
; XX
; PA   (GENZ ) GENZYME CORP.
; PA   (ROBE/) ROBERTS B L.
; PA   (SHAN/) SHANKARA S.
; XX
; PI   Roberts BL,  Shankara S;
; XX
; DR   WPI; 2000-106079/09.
; XX
; PT   Isolated polynucleotides differentially expressed between metastatic
; PT   and non-metastatic breast cancer cells, useful for diagnosis,
; PT   prevention and treatment of cancer -
; XX
; PS   Claim 1; Page 179; 219pp; English.
; XX
; CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct
; CC   transcripts that are preferentially transcribed in the metastatic breast
; CC   tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
; CC   AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
; CC   that are preferentially transcribed in the primary or non-metastatic
; CC   breast tumour tissue (i.e. are downregulated in metastatic breast tumour
; CC   cells). These transcripts can be used for diagnosis, prognosis,
; CC   monitoring and treatment of breast cancer, particularly where metastatic.
; CC   Diagnosis is by standard immunoassays or hybridisation/amplification
; CC   reactions. Compounds that modulate expression of the transcripts are
; CC   potentially useful for treatment of (metastatic) breast cancer, while
; CC   promoters from the transcripts are used to direct expression, in selected
; CC   cell types, of e.g. therapeutic genes (also ribozymes or antisense
; CC   sequences), particularly an antigen-encoding sequence for use in gene or
; CC   cell-based vaccines. Polypeptides encoded by the transcripts are also
; CC   useful in vaccines; for diagnosing breast cancer and for raising
; CC   specific antibodies (Ab). Ab are used to detect the polypeptides or as
; CC   therapeutic agents. Host cells that produce the polypeptides can be used
; CC   to expand and isolate populations of educated, antigen-specific immune
; CC   effecter cells, e.g. cytotoxic T lymphocytes, and these used for
; CC   adoptive immunotherapy.
; XX
; SQ   Sequence 10 BP; 2 A; 4 C; 3 G; 1 T; 0 other;
;
;  AAZ85236  Length: 10  October 2, 2003 14:58  Type: N  Check: 3825  ..
aaz85236

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3319 TTCAGGGG 3326
              ||||||||
Db          9 TTCAGGGG 2


RESULT 83
abk14251
;  TOIG of: abk14251  check: 4104  from: 1  to: 10
;
; ID   ABK14251 standard; DNA; 10 BP.
; XX
; AC   ABK14251;
; XX
; DT   08-MAY-2002  (first entry)
; XX
; DE   Human RRAS allele specific oligonucleotide (ASO) primer #15.
; XX
; KW   Primer; ss; human; RRAS; Ras; oncogene; SNP; single nucleotide;
; KW   polymorphism; viral oncogene; GTPase; cell growth; antisense;
; KW   drug development; cancer; allele specific oligonucleotide; ASO;
; KW   primer extension.
; XX
; OS   Homo sapiens.
; XX
; PN   WO200188201-A1.
; XX
; PD   22-NOV-2001.
; XX
; PF   17-MAY-2001; 2001WO-US16158.
; XX
; PR   17-MAY-2000; 2000US-204694P.
; XX
; PA   (GENA-) GENAISSANCE PHARM INC.
; XX
; PI   Chew A,  Choi JY,  Nandabalan K,  Sausker EA;
; XX
; DR   WPI; 2002-164141/21.
; XX
; PT   Isolated polynucleotide comprising a related RAS viral (r-ras) oncogene
; PT   homologue (RRAS) isogene (comprising defined polymorphism) useful for
; PT   providing haplotype information and drug screening  -
; XX
```

```
; PS   Claim 18; Page 12; 60pp; English.
; XX
; CC   This invention relates to genetic variants of the human related RAS
; CC   viral oncogene RRAS. Ras proteins are a member of a superfamily of small
; CC   GTPases that are involved in the regulation of cell growth. The
; CC   invention also comprises a related RAS viral (r-ras) oncogene homologue
; CC   (RRAS) isogene comprising one or more of the polymorphisms shown.
; CC   The sequences of the invention may be used to study the function of
; CC   RRAS or to treat disorders such as cancer using antisense therapy.
; CC   The polymorphic sequence of the invention is useful for providing
; CC   haplotype information of an individual. Furthermore, the polymorphic
; CC   sequence is useful for studying the biological function of RRAS as well
; CC   as identifying drugs targeting the protein for the treatment of
; CC   disorders related to its abnormal expression or function. In particular
; CC   for validating whether RRAS is a suitable target for drugs to treat
; CC   cancer, screening for such drugs and reducing bias in clinical trials.
; CC   The present sequence represents an allele specific oligonucleotide
; CC   primer #15 used to detect the human related RAS viral oncogene (RRAS)
; CC   polymorphisms of the invention using the primer extension technique.
; XX
; SQ   Sequence 10 BP; 2 A; 1 C; 5 G; 2 T; 0 other;
;
;  ABK14251  Length: 10  October 2, 2003 14:58  Type: N  Check: 4104  ..
abk14251

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3321 CAGGGGTT 3328
              ||||||||
Db          3 CAGGGGTT 10


RESULT 84
abk23538
;  TOIG of: abk23538  check: 3877  from: 1  to: 10
;
; ID   ABK23538 standard; DNA; 10 BP.
; XX
; AC   ABK23538;
; XX
; DT   09-APR-2002  (first entry)
; XX
; DE   Transcript tag DNA sequence #127 induced or suppressed by N-myc.
; XX
; KW   Myc-dependent downstream gene; neoplastic; cancer; growth; invasion;
; KW   spread; myc target; myc tag; SAGE; serial analysis of gene expression;
; KW   myc oncogene; N-myc; human neuroblastoma; cytostatic; ds.
; XX
; OS   Homo sapiens.
; XX
; PN   WO200185941-A2.
; XX
; PD   15-NOV-2001.
; XX
; PF   11-MAY-2001; 2001WO-NL00361.
; XX
; PR   11-MAY-2000; 2000EP-0201698.
; PR   29-JUN-2000; 2000EP-0202284.
; XX
; PA   (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.
; XX
; PI   Versteeg R,  Caron HN;
; XX
; DR   WPI; 2002-066603/09.
; XX
; PT   A new nucleic acid library of myc-dependent downstream genes capable of
; PT   supporting a neoplastic characteristic of cancer is useful to find new
; PT   therapies and diagnoses for cancer  -
; XX
; PS   Disclosure; Page 52; 69pp; English.
; XX
; CC   The present invention relates to a nucleic acid library comprising
; CC   myc-dependent downstream genes or their functional fragments essentially
; CC   capable of supporting a neoplastic character of cancer such as growth,
; CC   invasion or spread. These myc target or tag sequences are identified
; CC   by SAGE (serial analysis of gene expression). The library is useful to
; CC   find new diagnoses and treatments for cancer. The invention is also
; CC   useful to enhance production of recombinant proteins in a production
; CC   system with high expression of endogenous or transfected myc oncogenes.
; CC   ABK23412-ABK23828 represent transcript tag DNA sequences that are
; CC   activated or repressed by N-myc in human neuroblastoma.
; XX
; SQ   Sequence 10 BP; 2 A; 1 C; 4 G; 3 T; 0 other;
;
;  ABK23538  Length: 10  October 2, 2003 14:58  Type: N  Check: 3877  ..
abk23538

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3319 TTCAGGGG 3326
              ||||||||
Db          2 TTCAGGGG 9


RESULT 85
abk23629
;  TOIG of: abk23629  check: 3877  from: 1  to: 10
;
; ID   ABK23629 standard; DNA; 10 BP.
; XX
; AC   ABK23629;
; XX
; DT   09-APR-2002  (first entry)
; XX
; DE   Transcript tag DNA sequence #218 induced or suppressed by N-myc.
; XX
; KW   Myc-dependent downstream gene; neoplastic; cancer; growth; invasion;
; KW   spread; myc target; myc tag; SAGE; serial analysis of gene expression;
; KW   myc oncogene; N-myc; human neuroblastoma; cytostatic; ds.
; XX
; OS   Homo sapiens.
; XX
; PN   WO200185941-A2.
; XX
; PD   15-NOV-2001.
; XX
; PF   11-MAY-2001; 2001WO-NL00361.
; XX
; PR   11-MAY-2000; 2000EP-0201698.
; PR   29-JUN-2000; 2000EP-0202284.
; XX
; PA   (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.
; XX
; PI   Versteeg R,  Caron HN;
; XX
; DR   WPI; 2002-066603/09.
; XX
; PT   A new nucleic acid library of myc-dependent downstream genes capable of
; PT   supporting a neoplastic characteristic of cancer is useful to find new
; PT   therapies and diagnoses for cancer  -
; XX
; PS   Disclosure; Page 54; 69pp; English.
; XX
; CC   The present invention relates to a nucleic acid library comprising
; CC   myc-dependent downstream genes or their functional fragments essentially
; CC   capable of supporting a neoplastic character of cancer such as growth,
; CC   invasion or spread. These myc target or tag sequences are identified
; CC   by SAGE (serial analysis of gene expression). The library is useful to
; CC   find new diagnoses and treatments for cancer. The invention is also
; CC   useful to enhance production of recombinant proteins in a production
; CC   system with high expression of endogenous or transfected myc oncogenes.
; CC   ABK23412-ABK23828 represent transcript tag DNA sequences that are
```

```
; CC   activated or repressed by N-myc in human neuroblastoma.
; XX
; SQ   Sequence 10 BP; 2 A; 1 C; 4 G; 3 T; 0 other;
;
;  ABK23629  Length: 10  October 2, 2003 14:58  Type: N  Check: 3877  ..
abk23629

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3319 TTCAGGGG 3326
              ||||||||
Db          2 TTCAGGGG 9


RESULT 86
abk92637/c
;  TOIG of: abk92637  check: 3899  from: 1  to: 10
;
; ID   ABK92637 standard; DNA; 10 BP.
; XX
; AC   ABK92637;
; XX
; DT   20-AUG-2002  (first entry)
; XX
; DE   Primer-extension oligonucleotide #9 to detect human ADORA3 polymorphisms.
; XX
; KW   Human; single nucleotide polymorphism; SNP; ADORA3; haplotyping;
; KW   chromosome 1p21-p13; adenosine A3 receptor; genotyping;
; KW   pathophysiological heart condition; myocardial ischaemia;
; KW   chronic heart failure; primer; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   WO200236610-A2.
; XX
; PD   10-MAY-2002.
; XX
; PF   31-OCT-2001; 2001WO-US45718.
; XX
; PR   31-OCT-2000; 2000US-244626P.
; XX
; PA   (GENA-) GENAISSANCE PHARM INC.
; XX
; PI   Gilson CR,  Kazemi A,  Koshy B,  Monroe G;
; XX
; DR   WPI; 2002-489998/52.
; XX
; PT   Novel genetic variants of the adenosine A3 receptor, useful
; PT   therapeutically and in screening for drugs to treat diseases related to
; PT   ADORA3 activity e.g., myocardial ischaemia and chronic heart failure  -
; XX
; PS   Claim 17; Page 15; 82pp; English.
; XX
; CC   The present invention relates to novel single nucleotide polymorphisms
; CC   (SNPs) in the human adenosine A3 receptor (ADORA3) gene located on
; CC   chromosome 1p21-p13, and methods for haplotyping and/or genotyping
; CC   the ADORA3 gene. The methods of the invention make use of
; CC   allele-specific oligonucleotides (ASOs) as probes and primers and/or
; CC   primer-extension oligonucleotides for detecting the ADORA3 gene
; CC   polymorphisms. The polynucleotides and screened compounds are useful
; CC   for the treatment of diseases associated with ADORA3 activity, such as
; CC   pathophysiological conditions of the heart e.g. myocardial ischaemia
; CC   and chronic heart failure. ABK92629-ABK92654 represent primer-extension
; CC   oligonucleotides for detecting human ADORA3 gene polymorphisms.
; XX
; SQ   Sequence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 other;
;
;  ABK92637  Length: 10  October 2, 2003 14:58  Type: N  Check: 3899  ..
abk92637

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3318 ATTCAGGG 3325
              ||||||||
Db          8 ATTCAGGG 1


RESULT 87
abk96539/c
;  TOIG of: abk96539  check: 3838  from: 1  to: 10
;
; ID   ABK96539 standard; DNA; 10 BP.
; XX
; AC   ABK96539;
; XX
; DT   24-SEP-2002  (first entry)
; XX
; DE   Human PLAU gene, primer extension primer 3' terminus #12.
; XX
; KW   Human; ss; primer; Plasminogen activator; urokinase; PLAU; cancer;
; KW   cytostatic; serine protease; thrombolytic disorder; isogene; PCR;
; KW   pulmonary embolism; chromosome 10q24-qter; haplotype; genotype;
; KW   SNP; single nucleotide polymorphism; thrombolytic; gene therapy;
; KW   primer extension.
; XX
; OS   Homo sapiens.
; XX
; PN   WO200240503-A2.
; XX
; PD   23-MAY-2002.
; XX
; PF   14-NOV-2001; 2001WO-US44001.
; XX
; PR   17-NOV-2000; 2000US-249703P.
; XX
; PA   (GENA-) GENAISSANCE PHARM INC.
; XX
; PI   Anastasio AE,  Bentivegna SC,  Koshy B;
; XX
; DR   WPI; 2002-519370/55.
; XX
; PT   Genetic variants of Plasminogen activator, Urokinase (PLAU) isogenes,
; PT   useful for improving efficiency and reliability in drug development for
; PT   treating thrombolytic disorders and cancer -
; XX
; PS   Claim 16; Page 14; 92pp; English.
; XX
; CC   The invention relates to a polynucleotide comprising a first nucleotide
; CC   sequence (NS1) comprising a PLAU (plasminogen activator, urokinase,
; CC   a serine protease) isogene selected from isogenes 1-9 and 11-20 given
; CC   in the specification, where each isogene comprises the regions of the
; CC   PLAU gene or cDNA and is further defined by the corresponding sequence of
; CC   polymorphisms (defining single nucleotide polymorphisms, SNP). Also
; CC   included are methods of haplotyping/genotyping (and predicting the
; CC   haplotype/genotype of the  PLAU gene of an individual, identifying an
; CC   association between a trait and at least one haplotype or haplotype pair
; CC   of the PLAU gene, an isolated oligonucleotide for detecting a
; CC   polymorphism in the PLAU gene, a recombinant non-human organism
; CC   transformed or transfected with the gene or cDNA, fragments of the
; CC   polynucleotides of at least 10 base pairs encompassing a polymorphic
; CC   site, an isolated polymorphic variant PLAU protein or fragment, an
; CC   isolated monoclonal antibody specific for PLAU, a computer system for
; CC   storing and analysing polymorphism data for the PLAU gene and a genome
; CC   anthology for the PLAU gene. PLAU is useful in screening for drugs
; CC   targeting PLAU that are useful for treating thrombolytic disorders and
; CC   cancers. The methods are useful for improving the efficiency and
; CC   reliability of the discovery and development of drugs for treating
; CC   diseases associated with PLAU activity, in validating PLAU as a drug
; CC   target and in the design of clinical trials for treating a specific
; CC   condition of disease associated with PLAU activity. The antibody is
; CC   useful in diagnostic, prognostic and therapeutic methods. PLAU
; CC   polynucleotides are useful in studying the expression and function of
```

```
; CC   PLAU, and in expressing PLAU protein for use in screening for candidate
; CC   drugs to treat diseases related to PLAU activity. The gene for PLAU
; CC   is located on chromosome 10q24-qter. The present sequence is the 3'
; CC   terminus of an allele specific primer used to amplify PLAU
; CC   polynucleotides with a specific polymorphism using the technique of
; CC   primer extension.
; XX
; SQ   Sequence 10 BP; 2 A; 4 C; 2 G; 2 T; 0 other;
;
;  ABK96539  Length: 10  October 2, 2003 14:58  Type: N  Check: 3838  ..
abk96539

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3319 TTCAGGGG 3326
             ||||||||
Db          9 TTCAGGGG 2


RESULT 88
abt14312/c
;  TOIG of: abt14312  check: 3854  from: 1  to: 10
;
; ID   ABT14312 standard; DNA; 10 BP.
; XX
; AC   ABT14312;
; XX
; DT   20-FEB-2003  (first entry)
; XX
; DE   Nucleic acid PCR amplification method-related RAPD PCR primer #82.
; XX
; KW   Nucleic acid amplification; nucleic acid analysis; DNA analysis; ss;
; KW   RNA analysis; RAPD; PCR; primer; random amplified polymorphic DNA.
; XX
; OS   Unidentified.
; XX
; PN   WO200281743-A2.
; XX
; PD   17-OCT-2002.
; XX
; PF   28-MAR-2002; 2002WO-GB01489.
; XX
; PR   02-APR-2001; 2001GB-0008182.
; XX
; PA   (HAMI/) HAMILL B.
; XX
; PI   Hamill B;
; XX
; DR   WPI; 2003-075484/07.
; XX
; PT   Amplification of nucleotide sequences from polynucleotides by chain
; PT   extension of oligonucleotide primers, comprises 2 oligonucleotides in
; PT   solution, 2 attached to supports and both share complementary sequences
; PT   -
; XX
; PS   Disclosure; Fig 17; 60pp; English.
; XX
; CC   The invention comprises a method for the PCR amplification of nucleic
; CC   acids. The method involves a set of primers, where two of the primers are
; CC   in solution and at least two other primers are attached to a solid
; CC   support. The method of the invention can be used for the analysis of a
; CC   nucleic acid or a mixture of nucleic acids, including: single-stranded
; CC   DNA molecules, double-stranded DNA molecules and mRNA molecules. The
; CC   present DNA sequence represents a random amplified polymorphic DNA (RAPD)
; CC   PCR primer of the invention.
; XX
; SQ   Sequence 10 BP; 2 A; 5 C; 2 G; 1 T; 0 other;
;
;  ABT14312  Length: 10  October 2, 2003 14:58  Type: N  Check: 3854  ..
abt14312

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3320 TCAGGGGT 3327
             ||||||||
Db          9 TCAGGGGT 2


RESULT 89
aav04711/c
;  TOIG of: aav04711  check: 3169  from: 1  to: 9
;
; ID   AAV04711 standard; cDNA; 9 BP.
; XX
; AC   AAV04711;
; XX
; DT   05-JUN-1998  (first entry)
; XX
; DE   Delta-EKLF polypeptide recognition site.
; XX
; KW   Delta-globin promoter; delta-EKLF; erythroid Krueppel-like factor;
; KW   gene therapy; haematopoietic cell; sickle cell anaemia; beta-thalassemia;
; KW   ss.
; XX
; OS   Homo sapiens.
; XX
; PN   WO9747306-A1.
; XX
; PD   18-DEC-1997.
; XX
; PF   13-JUN-1997;   97WO-US10176.
; XX
; PR   14-JUN-1996;   96US-0019769.
; XX
; PA   (UABR-) UAB RES FOUND.
; XX
; PI   Donze D,  Townes TM;
; XX
; DR   WPI; 1998-052018/05.
; XX
; PT   Nucleic acid encoding an erythroid Krueppel-like factor that binds
; PT   the delta-globin promoter - used in gene therapy to increase
; PT   delta-globin expression for treatment of sickle cell anaemia and
; PT   beta-thalassemia
; XX
; PS   Claim 9; Page 36; 45pp; English.
; XX
; CC   This sequence represents the recognition site contained within the
; CC   delta-globin promoter for the delta-EKLF (erythroid Krueppel-like factor)
; CC   polypeptide (II) of the invention. DNA encoding (II) is used in gene
; CC   therapy to induce delta-globin gene expression, particularly in
; CC   haematopoietic cells, specifically for treating sickle cell anaemia and
; CC   beta-thalassemia. Increased expression of delta-globin increases
; CC   production of the HbA2 form of haemoglobin which has anti-sickling
; CC   activity. The DNA encoding (II) is introduced into cells in vivo or in
; CC   vitro. (II) can also be used to raise specific antibodies, useful for
; CC   measuring levels of (II) expression in treated patients. Since (II) is a
; CC   transcription factor, lower quantities of it are required compared with
; CC   other sorts of therapeutic gene products.
; XX
; SQ   Sequence 9 BP; 3 A; 3 C; 1 G; 2 T; 0 other;
;
;  AAV04711  Length: 9  October 2, 2003 14:58  Type: N  Check: 3169  ..
aav04711

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 2e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3314 AGGGATTCA 3322
             |||| ||||
Db          9 AGGGTTTCA 1
```

Search completed: October 2, 2003, 15:35:58
Job time : 1 secs